

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: July 2, 2004, 10:27:16 ; Search time 3991 Seconds
(without alignments)
10871.054 Million cell updates/sec

Title: US-09-247-874E-2_COPY_8345_9345
Perfect score: 1001
Sequence: 1 gctgtaccagagagagtcctg.....gcagacaaggtaacatgac 1001

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
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- 39: em_htgo_hum:*
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- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	997.8	99.7	9721	6	BD271230	BD271230 Predictio
2	997.8	99.7	9721	6	AX052806	AX052806 Sequence
3	997.8	99.7	9721	6	AX067266	AX067266 Sequence
4	997.8	99.7	9721	6	AX469435	AX469435 Sequence
5	997.8	99.7	9721	6	BD085856	BD085856 Methods o
6	997.8	99.7	9721	9	HSIL1B	X04500 Human gene
7	858.8	85.8	17447	9	AY137079	AY137079 Homo sapi
8	857.2	85.6	154214	9	AC079753	AC079753 Homo sapi
9	848.6	84.8	176373	6	BD080414	BD080414 Novel mol
10	834.6	83.4	7824	6	AX774856	AX774856 Sequence
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12	608	60.7	152331	6	BD080413	BD080413 Novel mol
13	605.8	60.5	614	11	G10509	G10509 human STS C
14	592.2	59.2	1522	9	BC008678	BC008678 Homo sapi
15	580.4	58.0	1473	9	HSPRO11B	X56087 Human mRNA
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18	580.2	58.0	1497	9	HUMIL1BA	M15330 Human inter
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36	385	38.5	492	6	AX753035	AX753035 Sequence
37	363.2	36.3	511	6	AX753048	AX753048 Sequence
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39	354.8	35.4	488	6	AX753040	AX753040 Sequence
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41	318.2	31.8	572	6	AX753038	AX753038 Sequence
42	307.6	30.7	451	6	AX339816	AX339816 Sequence
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45	232	23.2	1124	6	AR380763	AR380763 Sequence

ALIGNMENTS

RESULT 1
BD271230
LOCUS BD271230 9721 bp DNA linear PAT 17-JUL-2003
DEFINITION Prediction of risk of interstitial lung disease.
ACCESSION BD271230
VERSION BD271230.1 GI:33080998
KEYWORDS JP 2002540801-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9721)
AUTHORS Duff,G.W., Giovine,F.S.D. and Whyte,M.
TITLE Prediction of risk of interstitial lung disease
JOURNAL Patent: JP 2002540801-A 2 03-DEC-2002;

QY 301 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTTATTTATTTGTTT 360
Db 8645 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTTATTTATTTGTTT 8704
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RESULT 3
AX067266
LOCUS AX067266 9721 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 2 from Patent WO0100880.
ACCESSION AX067266
VERSION AX067266.1 GI:12544890
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Duff,G.W., Cox,A., Camp,N.J. and di Giovine,F.S.
TITLE Diagnostics and therapeutics for diseases associated with an il-1
inflammatory haplotype
JOURNAL Patent: WO 0100880-A 2 04-JAN-2001;
Interleukin Genetics, Inc. (US)
FEATURES
source
1..9721
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.7%; Score 997.8; DB 6; Length 9721;
Best Local Similarity 99.8%; Pred. No. 2e-236;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGPACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGSGCTGGCAGAAAGG 60
Db 8345 GCTGPACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGSGCTGGCAGAAAGG 8404
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RESULT 4
AX469435
LOCUS AX469435 9721 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 1 from Patent WO0222877.
ACCESSION AX469435
VERSION AX469435.1 GI:21901721
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hill, J.A., Wang, Z.C., Anderson, D.J. and Yunis, E.J.
TITLE Variants of il-1 beta gene and cd46 gene for diagnosing unexplained
recurrent pregnancy loss
JOURNAL Patent: WO 0222877-A 1 21-MAR-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); DANA-FARBER CANCER
INSTITUTE, INC. (US)
FEATURES
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/organism="Homo sapiens"
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ORIGIN
Query Match 99.7%; Score 997.8; DB 6; Length 9721;
Best Local Similarity 99.8%; Pred. No. 2e-236;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGTACCCAGAGAGTCCTGTGCTGATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 60
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RESULT 5
BD085856
LOCUS BD085856 9721 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods of diagnosing and treating chronic obstructive airway
diseases.
ACCESSION BD085856
VERSION BD085856.1 GI:22631466
KEYWORDS JP 2001522586-A/20.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 9721)
AUTHORS Duff, G.W., Giovain, M., Barnes, P.J. and Rim, S.
TITLE Methods of diagnosing and treating chronic obstructive airway
JOURNAL Patent: JP 2001522586-A 20 20-NOV-2001;
INTERLEUKIN GENETICS INC
COMMENT OS Unidentified
PN JP 2001522586-A/20
PD 20-NOV-2001
PF 09-NOV-1998 JP 2000519607
PR 07-NOV-1997 GB 9723553.5, 12-JAN-1998 US 09/005923 PI
GORDON W DUFF, MARKO GIOVAIN, PETER J BARNES, SIMON RIM PC
C12N15/09, C12Q1/68, C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Methods of diagnosing and treating chronic obstructive airway
diseases
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ORIGIN
Query Match 99.7%; Score 997.8; DB 6; Length 9721;
Best Local Similarity 99.8%; Pred. No. 2e-236;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 60
DB 8345 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 8404
QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTTTCTGTTGTCTACCAATGCC 120

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Db 9305 AGGAGAGGCAGCTAGTTATAAGCAGAACAGTAACATGAC 9345

RESULT 6

HSIL1B

LOCUS HSIL1B 9721 bp DNA linear PRI 26-JUN-1997

DEFINITION Human gene for prointerleukin 1 beta.

ACCESSION X04500

VERSION X04500.1 GI:33788

KEYWORDS interleukin 1 beta.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 9721)

AUTHORS Clark,B.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auron,P.E.

TITLE Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene

JOURNAL Nucleic Acids Res. 14 (20), 7897-7914 (1986)

MEDLINE 87040762

PUBMED 3490654

COMMENT Data kindly reviewed (13-MAY-1988) by Clark B.D.

FEATURES

Location/Qualifiers

1..9721

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/note="TATA-box like sequence"

1809..1816

1859..1866

1903..1909

1934..1953

1934..2005

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complement(1936..1943)

/note="pot. viral enhancer core sequence"

2006..2465

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2291..2297

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2458..2465

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CAAT signal

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intron

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ORIGIN

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RESULT 7
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DEFINITION Homo sapiens interleukin 1, beta (IL1B) gene, complete cds.
ACCESSION AY137079
VERSION AY137079.1 GI:22122009
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Rieder,M.J., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldane,S.A.,
AUTHORS Rajkumar,N.R., Toth,E.J., Yi,Q. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2002) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: SeattleSNPs. NHLBI HL66682 Program
for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
http://pga.gs.washington.edu).
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QY 841 GACTGGTAGTAACAGCTACCATGATTATTTATCTATCAATGCACCAAAACATCTGTTGAGCAAG 900
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Matches 963;	Conservative	0;	Mismatches 37;	Indels 12;	Gaps 7;
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QY	713	AGTACCTAGAAATATCCTTGGCCACCGAAGACTATCTCTCAACCCATCCCTTTATTTT	772		
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Db	8514	TGTTGTTCAACAGAGGATFATTCAGTGCACATCTGGAAACAGGATCAGCTGAAGCACTGCA	8573		

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-725J3. Actual start of this clone is at base position 1 of RP11-67L14; actual end is at base position 154214 of RP11-67L14.

There are polymorphic base differences in the overlap between RP11-67L14 and RP11-725J3.
Location/Qualifiers

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QY	601	AAAAAAGGGTCTCTCCTGATCATTTGACTGTCTGGATTGACACTGA---CAGTAAGC 656								
Db	45166	AAAAAAGGGTCTTCTCTGATCATTTGACTGTCTGGATTGACACTGAAGACATAAGACA 45107								
QY	657	AACAGGCTGTGAGAGTTCTTGGGGGACTAAAGCCCACTCTCTCATTTGCTGAGTGTGCA 712								
Db	45106	AACAGGCTGTGAGAGTTCTTGGGGGACTAAAGCCCACTCTCTCATTTGCTGAGTGTGCA 45047								
QY	713	AGTACCTAGAAATATCCTTGGCCACCGAAGACTATCTCTCACCCTATCCCTTTATTTT 772								
Db	45046	AGTACCTAGAAATATCCTTGGCCACCGAAGACTATCTCTCACCCTATCCCTTTATTTT 44987								
QY	773	GTTGTTCAACAGAAAGGATATTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCA 831								
Db	44986	GTTGTTCAACAGAAAGGATATTCAGTGCACATTTGGAACAGGATCAGCTGAAGCACTGCA 44927								
QY	832	GGGAGTCAGGACTGGTAGTAACAGCTACCA-TGATTTATCTATCAATGCACCAACATCT 890								
Db	44926	GGGAGTCAGGACTGGTAGTAACAGCTACCAAGTATTTATCTATCAATGCACCAACATCT 44867								
QY	891	GTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCC 950								
Db	44866	GTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCC 44807								
QY	951	CTCCTCAGATAGGAGGCGCTAGTTATAAGCAG-AACAAGGTAACATGAC 1001								
Db	44806	CTCCTCAGATAGGAGGCGCTAGTTATAAGCAGAAACAAGGTAACATGAC 44755								

RESULT 9
BD080414/c

LOCUS	BD080414	176373 bp	DNA	linear	PAT 27-AUG-2002			
DEFINITION	Novel molecules of the Tango-77 related protein family and uses thereof.							
ACCESSION	BD080414							
VERSION	BD080414.1	GI:22626017						
KEYWORDS	JP 2001512002-A/6.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1 (bases 1 to 176373)							
AUTHORS	Pan, Y.							
TITLE	Novel molecules of the Tango-77 related protein family and uses							
JOURNAL	Patent: JP 2001512002-A 6 21-AUG-2001; MILLENNIUM PHARMACEUTICALS INC							
COMMENT	OS Homo sapiens (human)							
	PN JP 2001512002-A/6							
	PD 21-AUG-2001							
	PF 03-AUG-1998 JP 2000505182							
	PR 04-AUG-1997 US 60/054646, 02-JUL-1998 US 60/091650 PI							
	YANG PAN							
	PC C12Q1/68, C07K14/52, C07K16/24, C12N5/10, C12N15/09, C12P21/02, PC C12Q1/02,							
	PC G01N33/15, G01N33/50, G01N33/53, G01N33/53, G01N33/566//A61K31/ PC 7088, A61K38/00,							
	PC A61P3/10, A61P11/06, A61P19/02, A61P29/00, A61P37/02, C12N5/00, PC C12N15/00,							
	PC A61K37/02							
	CC n = A, T, C or G							
	Key							
	Location/Qualifiers							
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	Best Local Similarity	95.8%;				Pred. No. 1.7e-199;		
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QY	1	GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60						
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QY	61	AACAGAAAGGTTTTTTCAGTACGGCTATAGCCTGGACTTTCCTGTGTGTCTACACCAATGCC 120						
Db	136149	AACAGAAAGGTTTTTTCAGTACGGCTATAGCCTGGACTTTCCTGTGTGTCTACACCAATGCC 136090						
QY	121	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180						
Db	136089	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 136030						
QY	181	CTCTCTCCTTTTCAGGGCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 240						
Db	136029	CTCTCTCCTTTTCAGGGCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 135970						
QY	241	CTACTCACTTAAAGCCCGCTGACAGAAACCAAGGCTTGGTTCTAAGAAACCCCTC 300						
Db	135969	CTACTCACTTAAAGCCCGCTGACAGAAACCAAGGCTTGGTTCTAAGAAACCCCTC 135910						
QY	301	TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTTATTTATTTGTTT 360						
Db	135909	TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTTATTTATTTGTTT 135850						
QY	361	GTTTGTGTTTGAATTCATTTGGTCTAATTTTAAAGGGGGCAAGAGTAGCAGTGTCTGTA 420						
Db	135849	GTTTGTGTTT-ATTTCATTTGGTCTAATTTTAAAGGGGGCAAGAGTAGCAGTGTCTGTA 135791						
QY	421	AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTCTCTCTT 480						
Db	135790	AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTCTCTCTT 135731						

QY 481 AAATCAAGTCCCTTAATTAACACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATA 540
Db 135730 AAATCAAGTCCCTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATA 135671
QY 541 TTTATAAATGAGCAAAATATGATACCTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 600
Db 135670 TTTATAAATGAGCAAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 135611
QY 601 AAAAAAAGGCTCTCTCTGATCATTGAC---TGCTGGATTGACACTGA---CAGTA 653
Db 135610 AAAAAA---GGCTCTCTCTGATCATTGACTTGCTTGGATTGACACTGAAGTAAG 135555
QY 654 AGCAACAGGCTGTGAGAGTTCTTGGG---ACTAAGCCCACTCCTCATTTGCTGAGTGCTG 710
Db 135554 ACAACAGGCTGTGAGAGTTCTTGGGGACTAAAGCCCACTCCTCATTTGCTGAGTGCTG 135495
QY 711 C-AAGTACCTAGAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCTTTAT 769
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QY 770 TTC-GTTGTTCAACAGAAAGGATATTCACTGTCACATCTGGAACAGGATCAGCTGAAGCACT 828
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RESULT 10
AX774856
LOCUS AX774856 7824 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 172 from Patent WO03038129.
ACCESSION AX774856
VERSION AX774856.1 GI:32486372
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Raponi,M.
TITLE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 172 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
FEATURES
Location/Qualifiers
source 1..7824
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ORIGIN

Query Match 83.4%; Score 834.6; DB 6; Length 7824;
Best Local Similarity 94.2%; Pred. No. 5.5e-196;
Matches 956; Conservative 0; Mismatches 44; Indels 15; Gaps 8;
QY 1 GCTGTACCCAGAGAGTCCCTGCTGAATGTGAGTCAATCCCTAGGCTGGCAGAAAGGG 60
Db 6788 GCTGTACCCAGAGAGTCCCTGCTGAATGTGAGTCAATCCCTAGGCTGGCAGAAAGGG 6847
QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCTGTTGCTACACCAATGCC 120
Db 6848 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCTGTTGCTACACCAATGCC 6907

QY 121 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
Db 6908 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 6967
QY 181 CTCTCTCCTTTTCAGG3CCAATCCCCAGCCCTTTTGTGAGCCAGG3CCTCTCTCACCTCTC 240
Db 6968 CTCTCTCCTTTTCAGG3CCAATCCCCAGCCCTTTTGTGAGCCAGG3CCTCTCTCACCTCTC 7027
QY 241 CTACTCACTTAAAGCCCGCCTGACAGAAACCAACGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db 7028 CTACTCACTTAAAGCCCGCCTGACAGAAACCAACGGCCACATTTGGTTCTAAGAAACCCCTC 7087
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Db 7088 TGTCAATTCGCTCCACATCTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT 7147
QY 361 GTTTGTTTGTGATTCAATTTGTTCTAATTTTATTTCAAGGGGGGCAAGAGTAGCAGTGTCTGTA 420
Db 7148 GTTTGTTT -ATTCAATTTGTTCTAATTTTATTTCAAGGGGGGCAAGAGTAGCAGTGTCTGTA 7206
QY 421 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTGCTCTCTTT 480
Db 7207 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTGCTCTCTTT 7266
QY 481 AAATCAAGTCCCTTAAATTAACACTGAAATATATTAAGCTCAGATTATTTAAATGGGAATA 540
Db 7267 AAATCAAGTCCCTTAAATTAAGACTGAAATATATTAAGCTCAGATTATTTAAATGGGAATA 7326
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QY 713 A--GTACCTAGAAATAT-CCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCTTTAT 769
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QY 770 TTC-GTTGTTCAACAGAAAGGATATTCACTGTCACATCTGGAACAGGATCAGCTGAAGCACT 828
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QY 888 TCTGTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCAACAAG 947
Db 7687 TCTGTTGAGCAAGCGCTATGTACGAGGAGCTGGGAGTACAGAGATGAGAAACAGTCAACAAG 7746
QY 948 TCCCTCCTCAGATAGGAGGAGGAGCTAGTTATAAGCAG-AACAAGGTAACATGAC 1001
Db 7747 TCCCTCCTCAGATAGGAGGAGGAGCTAGTTATAAGCAGAAACAAGGTAACATGAC 7801

RESULT 11

HUMIL1B
LOCUS Human interleukin 1-beta (IL1B) gene, complete cds.
DEFINITION
ACCESSION M15840
VERSION M15840.1 GI:186281
KEYWORDS Alu repeat; interleukin 1-beta.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7824)

AUTHORS Bensi,G., Raugai,G., Palla,E., Carinci,V., Tornese Buonamassa,D. and Melli,M.
TITLE Human interleukin-1 beta gene
JOURNAL Gene 52 (1), 95-101 (1987)
MEDLINE 87248099
PUBMED 2954882
REFERENCE 2 (bases 1 to 7824)
AUTHORS Bensi,G.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1987) G. Bensi, Sclavo Research Center, Siena, Italy
COMMENT Original source text: Human DNA.
FEATURES
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prim_transcript 374..7380
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446..908
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/note="interleukin-1 beta; G00-120-094"
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6570..6782
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number=7
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ORIGIN 242 bp upstream of HindIII site; chromosome 2q13-q21.
Query Match 83.4%; Score 834.6; DB 9; Length 7824;
Best Local Similarity 94.2%; Pred. No. 5.5e-196;
Matches 956; Conservative 0; Mismatches 44; Indels 15; Gaps 8;
QY 1 GCTGTACCCAGAGAGTCTCTGTCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 60
DB 6788 GCTGTACCCAGAGAGTCTCTGTCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 6847
QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCCTGTTGTCTACACCAATGCC 120
DB 6848 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCCTGTTGTCTACACCAATGCC 6907
QY 121 CAACTGCCTGCTTAGGGTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
DB 6908 CAACTGCCTGCTTAGGGTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 6967
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DB 7148 GTTTGTTTTCATTCATTTGTTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 7206
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ORIGIN
Query Match 59.2%; Score 592.2; DB 9; Length 1522;
Best Local Similarity 99.3%; Pred. No. 6.7e-136;
Matches 605; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 60
Db |||||
QY 903 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 962
Db |||||
QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTCCTGTTGTCTACACCAATGCC 120
Db |||||
QY 963 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTCCTGTTGTCTACACCAATGCC 1022
Db |||||
QY 121 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
Db |||||
QY 1023 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 1082
Db |||||
QY 181 CTCTCTCCTTTAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 240
Db |||||
QY 1083 CTCTCTCCTTTAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 1142
Db |||||
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 300
Db |||||
QY 1143 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 1202
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QY 1263 GTTTGTTT -ATTCAATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA 1321
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Db |||||
QY 1382 AAATCAAGTCCTTTTAATTAAGACTGAAATATATAAGCTCAGATTATTATTAATGGGAATA 1441
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QY 1442 TTTATAAATGAGCAAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 1501
Db |||||
QY 601 AAAAAAAAA 609
Db |||||

Db 1502 AAAAAAAAA 1510

RESULT 15
HSPROI1B
LOCUS 1473 bp mRNA linear PRI 06-DEC-1990
DEFINITION Human mRNA for prointerleukin 1 beta.
ACCESSION X56087
VERSION X56087.1 GI:35662
KEYWORDS prointerleukin 1; prointerleukin 1 beta.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Kotenko,S.V., Buleikov,M.T., Veiko,V.P., Epishin,S.M.,
Lomakin,I.B., Emel'yanov,A.V., Kozlov,A.P., Konusova,V.G.,
Kotov,A.Y., Kurbatova,T.V., Reshetnikov,V.L., Simbirtsev,A.S.,
Ketlinskii,S.A. and Vinetskii,Y.P.
TITLE Cloning of the cDNA coding for human prointerleukin-1 alpha and
prointerleukin-1 beta
JOURNAL Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989)
MEDLINE 90249285
PUBMED 2635664
FEATURES
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58. .864
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/product="prointerleukin-1 beta"

ORIGIN
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Best Local Similarity 98.8%; Pred. No. 5.6e-133;
Matches 595; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Db |||||
QY 873 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 932
Db |||||
QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTCCTGTTGTCTACACCAATGCC 120
Db |||||
QY 933 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTCCTGTTGTCTACACCAATGCC 992
Db |||||
QY 121 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
Db |||||
QY 993 CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 1052
Db |||||
QY 181 CTCTCTCCTTTAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 240
Db |||||
QY 1053 CTCTCTCCTTTAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 1112
Db |||||
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db |||||

Db	1113	CTACTCACTTAAAGCCCGCTGACAGAAACCCACGGCCACATTTGGTTCTAAGAAACCCCTC	1172
Qy	301	TGTCATTGCGTCCACACATTCTGATGAGCAACCGTTCCCTATTATTTATTTATTTGTTT	360
Db	1173	TGTCATTGCGTCCACACATTCTGATGAGCAACCGTTCCCTATTATTTATTTATTTGTTT	1232
Qy	361	GTITGTTTGTGATTCAATTTGGTCTTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA	420
Db	1233	GTITGTTT-ATTCAATTTGGTCTTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA	1291
Qy	421	AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTT	480
Db	1292	AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTT	1351
Qy	481	AAATCAAGTCCTTTAAATTAACACTGAAATATATATAAGCTCAGATTATTAAATGGGAATA	540
Db	1352	AAATCAAGTCCTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATA	1411
Qy	541	TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA	600
Db	1412	TTTATAAATGAGCAAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA	1471
Qy	601	AA 602	
Db	1472	AA 1473	

Search completed: July 2, 2004, 12:34:03
Job time : 3999 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 09:35:39 ; Search time 458 Seconds
(without alignments)
9284.817 Million cell updates/sec

Title: US-09-247-874E-2_COPY_8345_9345
Perfect score: 1001
Sequence: 1 gctgtaccacagagagtctg.....gcagacaaggtaacatgac 1001

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999.4	99.8	9721	3	AAA50175 Human int
2	997.8	99.7	9721	2	AAX75924 Human int
3	997.8	99.7	9721	2	ABX15529 Human int
4	997.8	99.7	9721	3	AAA34823 Human ade
5	997.8	99.7	9721	3	AAA50174 Human int
6	997.8	99.7	9721	3	AAF20945 Human int
7	997.8	99.7	9721	3	AAC63768 Human IL-
8	997.8	99.7	9721	5	AAC91434 Human IL-
9	997.8	99.7	9721	6	AAD35192 Human pro
10	997.8	99.7	9721	7	ABZ96639 Human int
11	997.8	99.7	9721	7	AAD51464 Human int
12	997.8	99.7	9721	7	AAL54516 Interleuk
13	997.8	99.7	15402	7	ACC83528 Human int
14	997.8	99.7	29433	3	AAA34828 Human ade
15	997.8	99.7	29433	3	AAF20950 Human int
16	997.8	99.7	29433	7	ABZ96644 Human nuc
17	997.8	99.7	209273	7	AAF21437 Human fac
18	997.8	99.7	209274	7	ABZ97131 Human enz
19	988.2	98.7	9721	4	AAF27666 IL-1B DNA
20	848.6	84.8	14690	2	AAX22303 Human IL-
21	834.6	83.4	7824	2	AAQ74052 Human int
22	834.6	83.4	7824	4	AAH24368 Human IL1
23	834.6	83.4	7824	9	ADE84953 Farnesyl

24	833	83.2	7824	6	ABK50291	Abk50291 Human int
25	832.6	83.2	7824	6	ABK50293	Abk50293 Human int
26	608	60.7	8639	2	AAX02995	Aax02995 Human IL-
27	589.8	58.9	1638	9	ADE25711	Ade25711 Human CDN
28	587.8	58.7	1541	7	ABX63544	Abx63544 Human CDN
29	580.2	58.0	1497	3	AAA34822	Aaa34822 Human ade
30	580.2	58.0	1497	3	AAF20944	Aaf20944 Human int
31	580.2	58.0	1497	6	ABK83933	Abk83933 Human CDN
32	580.2	58.0	1497	7	ABZ96638	Abz96638 Human int
33	580.2	58.0	1497	7	ACA64833	Aca64833 Human IL-
34	580.2	58.0	1497	9	ADD18661	Add18661 Human dis
35	577	57.6	1497	2	AAQ58462	Aaq58462 IL-1 beta
36	565	56.4	1743	6	ABS62745	Abs62745 Prostate
37	565	56.4	1743	7	ACA03937	Aca03937 CDNA down
38	563.4	56.3	1744	9	ADB47542	Adb47542 Human CDN
39	561.4	56.1	1507	1	AAN50060	Aan50060 Sequence
40	561.4	56.1	1507	2	AAQ50981	Aaq50981 Human int
41	554.8	55.4	1382	6	ABL46348	Ab146348 Human int
42	553.6	55.3	656	3	AAA51659	Aaa51659 Interleuk
43	553.6	55.3	1496	3	AAA34824	Aaa34824 Human ade
44	553.6	55.3	1496	3	AAF20946	Aaf20946 Human int
45	553.6	55.3	1496	7	ABZ96640	Abz96640 Human int

ALIGNMENTS

RESULT 1
AAA50175
ID AAA50175 standard; DNA; 9721 BP.
XX
AC AAA50175;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human interleukin-1 beta allele 2 (+6912).
XX
KW Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;
KW coronary artery disease; osteoporosis; nephropathy; alopecia areata;
KW Graves disease; systemic lupus erythematosus; lichen sclerosis;
KW ulcerative colitis; diabetic retinopathy; periodontal disease;
KW juvenile chronic arthritis; psoriasis; insulin dependent diabetes;
KW asthma; lung fibrosis; chronic inflammatory liver disease;
KW rheumatoid arthritis; chronic inflammatory lung disease;
KW antiinflammatory; osteopathic; dermatological; immunosuppressive;
KW antidiabetic; antithyroid; antiarthritic; antirheumatic; antiasthmatic;
KW antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(8904,C)
FT /*tag= a
FT /note= "IL-1B allele 2 (+6912)"
XX
PN WO200047619-A1.
XX
PD 17-AUG-2000.
XX
PF 10-FEB-2000; 2000WO-US003443.
XX
PR 10-FEB-1999; 99US-00247874.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Duff GW, Di Giovine FS;
XX
DR WPI; 2000-558192/51.
XX
PT Novel methods and nucleic acids for diagnosing and treating disorders
PT associated with high levels of interleukin 1beta, especially inflammatory
PT diseases.
XX

Claim 34; Fig 2; 74pp; English.

The present sequence is that of human interleukin-1 beta (IL-1B) allele 2 (+6912), which is a form of the IL-1B gene that contains guanine at position +6912; IL-1B allele 1 (+6912) has cytosine at this position (see AA50174). The invention is based on the identification of this novel allele at marker +6912 of the IL-1B gene. The C to G transition occurs within the 3' untranslated region of the IL-1B gene and results in an increased level of IL-1B protein. Individuals homozygous for the IL-1B allele 2 (+6912) accumulate approximately 4 times more immunoreactive IL-1B protein than homozygotes for IL-1B allele 1 (+6912). Methods and kits are provided for detecting IL-1B allele 2 (+6912), or an allele in linkage disequilibrium with an IL-1B allele 2 (+6912), and thereby determining a patient's susceptibility to developing inflammatory disorders, especially coronary artery disease, osteoporosis, nephropathy in diabetes mellitus, alopecia areata, Graves disease, systemic lupus erythematosus, lichen sclerosis, ulcerative colitis, diabetes, retinopathy, periodontal disease, juvenile chronic arthritis, psoriasis, insulin dependent diabetes, asthma, chronic inflammatory liver disease, chronic inflammatory lung disease, lung fibrosis, and rheumatoid arthritis (claimed). Identification of the IL-1B allele 2 (+6912) and its involvement in IL-1B overproduction also enables screening assays for identifying IL-1B antagonists that can be used to treat conditions associated with IL-1B allele 2 (+6912). Transgenic animals are also claimed, and can be used to identify IL-1B agonists and antagonists, or to confirm the safety and efficacy of candidate therapeutics

Sequence 9721 BP; 2661 A; 2327 C; 2123 G; 2608 T; 0 U; 2 Other;

Query Match 99.8%; Score 999.4; DB 3; Length 9721;
Best Local Similarity 99.9%; Pred. No. 3.1e-235;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GCTGTACCCAGAGATCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCAGAAAGGG 60
8345 GCTGTACCCAGAGATCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCAGAAAGGG 8404
61 AACAGAAAGTGTGAGTACGGCTATAGCTGGACTTCTCTGTTGTCTACACCAATGCC 120
8405 AACAGAAAGTGTGAGTACGGCTATAGCTGGACTTCTCTGTTGTCTACACCAATGCC 8464
121 CAACCTGCCTTAGGGTAGTGTGAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
8465 CAACCTGCCTTAGGGTAGTGTGAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 8524
181 CTCTCTCTTTTCCAGGGCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 240
8525 CTCTCTCTTTTCCAGGGCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 8584
241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 300
8585 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 8644
301 TGTCACTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
8645 TGTCACTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704
361 GTTTGTTTGTGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 420
8705 GTTTGTTTGTGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 8764
421 AAAGAGCCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 480
8765 AAAGAGCCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 8824
481 AAATCAAGTCTTTTAAATTAACACTGAAATATATATAGCTCAGATTATTTAAATGGGATA 540
8825 AAATCAAGTCTTTTAAATTAACACTGAAATATATATAGCTCAGATTATTTAAATGGGATA 8884
541 TTTATAATGAGCAAAATATGATACCTGTTCAATGGTTCTGAAATAAATCTTCACTGAAGAA 600
8885 TTTATAATGAGCAAAATATGATACCTGTTCAATGGTTCTGAAATAAATCTTCACTGAAGAA 8944

601 AAAAAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC 560
8945 AAAAAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC 9004
661 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 720
9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 9064
721 GAAATATCTTGGCCACCCGAGACTATCTCTCCTCACCCTATCCCTTTATTTGTTTCA 780
9065 GAAATATCTTGGCCACCCGAGACTATCTCTCCTCACCCTATCCCTTTATTTGTTTCA 9124
781 ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGACGGAGTCAG 840
9125 ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGACGGAGTCAG 9184
841 GACTGTTAGTAACAGCTACCATGATTTATCTATCAATGACCAACATCTGTTGAGCAAG 900
9185 GACTGTTAGTAACAGCTACCATGATTTATCTATCAATGACCAACATCTGTTGAGCAAG 9244
901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCCTCAGAT 960
9245 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCCTCAGAT 9304
961 AGGAGAGGAGCTAGTTATATAGCAAGCAAGGTAACATGAC 1001
9305 AGGAGAGGAGCTAGTTATATAGCAAGCAAGGTAACATGAC 9345

RESULT 2
AAAX75924

ID AAX75924 standard; DNA; 9721 BP.

XX

AC AAX75924;

XX

DT 29-JUL-1999 (first entry)

XX

DE Human interleukin 1B gene.

XX

KW Human; interleukin 1; IL-1B; IL-1A; IL-1RN; diagnosis; detection;
KW chronic obstructive airway disease; chronic bronchitis; emphysema;
KW asthma; chronic bronchiolitis; proinflammatory haplotype; SS.

XX

OS Homo sapiens.

XX

PN WO9924615-A2.

XX

PD 20-MAY-1999.

XX

PF 09-NOV-1998; 98WO-US023721.

XX

PR 07-NOV-1997; 97GB-00023553.

XX

PR 12-JAN-1998; 98US-00005923.

XX

PA (MEDI-) MEDICAL SCI SYSTEMS INC.

XX

PI Duff GW, Giovine M, Barnes PJ, Lim S;

XX

DR WPI; 1999-327420/27.

XX

PT Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory
PT haplotype alleles, useful for predicting susceptibility to developing
PT chronic obstructive airway disease.

XX

PS Example 1; Fig 2; 37pp; English.

XX

CC The present invention describes genotyping a nucleic acid sample from a
CC subject to determine at least one allele of an interleukin-1 (IL-1)
CC proinflammatory haplotype. A method has also been described for
CC determining a subject's susceptibility to developing chronic obstructive
CC airway disease (COAD) or for predicting the rapidity or ultimate
CC progression of a COAD in the subject by: (a) obtaining a nucleic acid
CC sample from the subject; and (b) detecting at least one allele of an IL-1

CC proinflammatory haplotype in the sample, where detection of at least one
CC of these alleles indicates that the patient has an increased
CC susceptibility to developing COAD. The method is useful for determining
CC the susceptibility of subjects to developing chronic obstructive airway
CC disease or for predicting the rapidity or ultimate progression of chronic
CC obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic
CC bronchitis or chronic bronchiolitis. The method provides for early
CC identification of chronic obstructive airway disease (COAD), facilitating
CC administration of appropriate treatment at the earliest stage, thereby
CC increasing the probability of a positive outcome. The present sequence
CC represents the human IL-1B gene
XX
SQ Sequence 9721 BP; 2662 A; 2328 C; 2121 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 2; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	GCTGTACCCAGAGTCTCTGTCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	60
Db	8345	GCTGTACCCAGAGTCTCTGTCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	8404
QY	61	AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACACCAATGCC	120
Db	8405	AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACACCAATGCC	8464
QY	121	CAACTGCCTGCCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	180
Db	8465	CAACTGCCTGCCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	8524
QY	181	CTCTCTCCTTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTGAGCAGGCCTCTCTCACCTCTC	240
Db	8525	CTCTCTCCTTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTGAGCAGGCCTCTCTCACCTCTC	8584
QY	241	CTACTCACTTAAAGCCCGCCTGACAGAAACACCGCCACATTGGTTCTAAGAAACCCCTC	300
Db	8585	CTACTCACTTAAAGCCCGCCTGACAGAAACACCGCCACATTGGTTCTAAGAAACCCCTC	8644
QY	301	TGTCATTGCTCCACATTTCTGATGACCAACCGCTTCCCTATTATTTATTTATTGTTT	360
Db	8645	TGTCATTGCTCCACATTTCTGATGACCAACCGCTTCCCTATTATTTATTTATTGTTT	8704
QY	361	GTTTGTGTTTGCATTTGCTTAATTTATTTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA	420
Db	8705	GTTTGTGTTTGCATTTGCTTAATTTATTTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA	8764
QY	421	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTT	480
Db	8765	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTT	8824
QY	481	AAATCAAGTCCTTTAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA	540
Db	8825	AAATCAAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA	8884
QY	541	TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAA	600
Db	8885	TTTATAAATGAGCAAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAA	8944
QY	601	AAAAAAAGGGTCTCTCCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC	660
Db	8945	AAAAAAAGGGTCTCTCCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC	9004
QY	661	AGGCTGTGAGAGTTCTTGGGACTTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA	720
Db	9005	AGGCTGTGAGAGTTCTTGGGACTTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA	9064
QY	721	GAAATATCCTTGGCCACCGAAGACTATCCTCTCACCCATCCCTTTATTTGTTTCA	780
Db	9065	GAAATATCCTTGGCCACCGAAGACTATCCTCTCACCCATCCCTTTATTTGTTTCA	9124
QY	781	ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGAGGGAGTCAG	840
Db	9125	ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGAGGGAGTCAG	9184

QY	841	GACTGTAGTAACAGCTACCATGATTATCTATCAATGCACCAACATCTGTTGAGCAAG	900
Db	9185	GACTGTAGTAACAGCTACCATGATTATCTATCAATGCACCAACATCTGTTGAGCAAG	9244
QY	901	CGCTATGTACTAGGAGCTGGAGTACAGAGATGAGAACAGTCACAAGTCCCTCCTCAGAT	960
Db	9245	CGCTATGTACTAGGAGCTGGAGTACAGAGATGAGAACAGTCACAAGTCCCTCCTCAGAT	9304
QY	961	AGGAGAGGCAGCTAGTTATAAGCAGAACAAAGGTAACATGAC	1001
Db	9305	AGGAGAGGCAGCTAGTTATAAGCAGAACAAAGGTAACATGAC	9345

RESULT 3

ABX15529

ID ABX15529 standard; DNA; 9721 BP.

XX ABX15529;

DT 11-APR-2003 (first entry)

XX Human interleukin-1B, IL-1B, gene.

Human; ds; gene; interleukin-1B; IL-1B; chromosome 2q13; nephropathy;
inflammatory disease; Systemic Inflammatory Response; SIRS;
Alzheimer's disease; arthritis; acute joint inflammation; ophthalmopathy;
juvenile chronic arthritis; asthma; bronchial asthma; pulmonary disease;
chronic obstructive airways disease; cardiovascular disease; thyroditis;
atherosclerosis; autoimmune carditis; cardiomyopathy; ulcerative colitis;
cardiac cell dysfunction; aortic smooth muscle cell activation; trauma;
cardiac cell apoptosis; gastrointestinal inflammation; cerebral trauma;
inflammatory bowel disease; HIV infection; coronary artery lesion;
Kawasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy;
glomerulonephritis; diabetic retinopathy; Grave's ophthalmopathy;
osteoporosis; bone loss; otitis media; pancreatitis; periodontal disease;
chronic lung disease; chronic sinusitis; chronic lymphocytic thyroiditis;
urinary tract infection; chronic prostatitis; immunological disorder;
chronic pelvic pain syndrome; alopecia areata; Grave's disease;
thyroid disease; goiter; struma lymphomatosa; sleep disorder; neoplasia;
chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis;
Leprosy; myocardial dysfunction; breast cancer; organ transplant;
Hodgkin's disease; hormonal regulation; fertility; septicaemia.

XX Homo sapiens.

XX US2002146700-A1.

XX 10-OCT-2002.

XX 27-APR-2001; 2001US-00845129.

XX 29-MAY-1997; 97GB-00011040.

XX 30-JUN-1999; 99US-00345217.

XX (INTE-) INTERLEUKIN GENETICS INC.

PI Duff GW, Cox A, Camp NJ, Di Giovine FS;

XX WPI; 1999-080814/07.

XX New method of determining a patient's susceptibility to inflammatory
disorders - by detecting the presence of an IL-1 (44112332) haplotype,
useful in designing treatment strategies that modulate the activity of
proteins produced by the IL-1 gene cluster.

XX Disclosure; Fig 4; 42pp; English.

CC The invention relates to a method for determining whether a subject has
or is predisposed to developing a disease or condition that is associated
with an IL-1 inflammatory haplotype. The method involves detecting at
least one allele of the haplotype, where the presence of the allele
indicates that the subject is predisposed to the development or has the

disease or condition. The invention allows the determination of an individual's likelihood for developing a particular disease or condition associated with interleukin 1 (IL-1) polymorphisms without necessarily determining or characterising the causative genetic variation. Diseases such as inflammatory disease e.g. Systemic Inflammatory Response (SIRS), Alzheimer's disease; arthritis e.g. acute joint inflammation, juvenile chronic arthritis; asthma e.g. bronchial asthma, chronic obstructive airways disease; cardiovascular diseases e.g. atherosclerosis, autoimmune carditis; cardiomyopathy and cardiac cell dysfunction e.g. aortic smooth muscle cell activation, cardiac cell apoptosis; gastrointestinal inflammation e.g. inflammatory bowel disease; ulcerative colitis; HIV infection; Kawasaki's syndrome e.g. cervical lymphadenopathy, coronary artery lesions; nephropathies e.g. diabetic nephropathy, Grave's ophthalmopathy; osteoporosis e.g. bone loss, otitis media; pancreatitis; periodontal disease; pulmonary diseases e.g. chronic lung disease, chronic sinusitis; thyroiditis e.g. chronic lymphocytic thyroiditis; urinary tract infections e.g. chronic prostatitis, chronic pelvic pain syndrome; immunological disorders e.g. alopecia areata, Graves disease; thyroid diseases e.g. goiter, struma lymphomatosa; sleep disorders; chronic fatigue syndrome; obesity; infectious diseases e.g. Leprosy, Leishmaniasis; trauma e.g. cerebral trauma, myocardial dysfunction; neoplasias e.g. breast cancer, Hodgkin's disease; hormonal regulation e.g. fertility, septicaemia; organ transplants. This allows for a more customised approach to preventing the onset or progression of the disease or condition, e.g. a clinician can more effectively prescribe a therapy that will address the molecular basis of the disease or condition. The present sequence represents the sequence of the human interleukin-1B gene located on chromosome 2q13

Sequence 9721 BP; 2661 A; 2329 C; 2121 G; 2608 T; 0 U; 2 Other;

QY	1	GCTGTACCCAGAGATCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	60
Db	8345	GCTGTACCCAGAGATCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	8404
QY	61	AACAGAAAGTTTGTAGTACGGCTATAGCCTGGACTTCCTGTTGTCTACACCAATGCC	120
Db	8405	AACAGAAAGTTTGTAGTACGGCTATAGCCTGGACTTCCTGTTGTCTACACCAATGCC	8464
QY	121	CAACTGCCCTGCTAGGGTAGTGTGAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	180
Db	8465	CAACTGCCCTGCTAGGGTAGTGTGAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	8524
QY	181	CTCTCTCCTTTCAGGGCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTACCTCTC	240
Db	8525	CTCTCTCCTTTCAGGGCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTACCTCTC	8584
QY	241	CTACTCACTTAAAGCCCGCCTGACAGAAACACCGGCCACATTTGGTTCTTAAGAAACCCCTC	300
Db	8585	CTACTCACTTAAAGCCCGCCTGACAGAAACACCGGCCACATTTGGTTCTTAAGAAACCCCTC	8644
QY	301	TGTCATTGCTCCACATCTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT	360
Db	8645	TGTCATTGCTCCACATCTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT	8704
QY	361	GTTTGTGTTTGAATTCATTGCTTAATTTATTCAAGGGGGGCAAGTAGCAGTCTCTGTA	420
Db	8705	GTTTGTGTTTGAATTCATTGCTTAATTTATTCAAGGGGGGCAAGTAGCAGTCTCTGTA	8764
QY	421	AAAGAGCCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTT	480
Db	8765	AAAGAGCCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTT	8824
QY	481	AAATCAAGTCCCTTAAATTAACACTGAAATATATAGCTCAGATTTTAAATGGGAATA	540
Db	8825	AAATCAAGTCCCTTAAATTAAGACTGAAATATATAGCTCAGATTTTAAATGGGAATA	8884
QY	541	TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAA	600

Db	8885	TTTATAAATGAGCAAAATATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAA	8944
QY	601	AAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAC	660
Db	8945	AAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAC	9004
QY	661	AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCTCATTTGCTGAGTCTGCAAGTACCTA	720
Db	9005	AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCTCATTTGCTGAGTCTGCAAGTACCTA	9064
QY	721	GAAATATCCTTGGCCACCGAAGACTATCTCTCCTCACCCTTATTTGTTGTTCA	780
Db	9065	GAAATATCCTTGGCCACCGAAGACTATCTCTCCTCACCCTTATTTGTTGTTCA	9124
QY	781	ACAGAAGGATATTGAGTGACATCTGGAACAGGATCAGCTGAAGCACTGCGAGGAGTCAG	840
Db	9125	ACAGAAGGATATTGAGTGACATCTGGAACAGGATCAGCTGAAGCACTGCGAGGAGTCAG	9184
QY	841	GACTGTGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG	900
Db	9185	GACTGTGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG	9244
QY	901	CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAAAGTCCCTCTCAGAT	960
Db	9245	CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAAAGTCCCTCTCAGAT	9304
QY	961	AGGAGAGGCGAGCTAGTTATAGCAGAAACAAGGTAACATGAC	1001
Db	9305	AGGAGAGGCGAGCTAGTTATAGCAGAAACAAGGTAACATGAC	9345

RESULT 4
AAA34823
ID AAA34823 standard; DNA; 9721 BP.
XX
AC AAA34823;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2512.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.
XX
PS Disclosure; Page 673-675; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match	99.7%;	Score 997.8;	DB 3;	Length 9721;
Best Local Similarity	99.8%;	Pred. No. 7.8e-235;		
Matches 999;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY	1	GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAAGG	60
Db	8345		
		GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAAGG	8404
QY	61	AACAGAAAGGTTTTTTGAGTAAGGCTATAGCCCTGGACTTCCTGTTGCTACACCAATGCC	120
Db	8405		
		AACAGAAAGGTTTTTTGAGTAAGGCTATAGCCCTGGACTTCCTGTTGCTACACCAATGCC	8464
QY	121	CAACTGCCTGCCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCGAGGACAGTCAG	180
Db	8465		
		CAACTGCCTGCCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCGAGGACAGTCAG	8524
QY	181	CTCTCTCCTTTTCAGGGCCAATCCCCAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC	240
Db	8525		
		CTCTCTCCTTTTCAGGGCCAATCCCCAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC	8584
QY	241	CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGSCACATTGTGTTCTAAGAAACCCCTC	300
Db	8585		
		CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGSCACATTGTGTTCTAAGAAACCCCTC	8644
QY	301	TGTCATTGCTCCCACATTCTGATGAGCAAACCGCTTCCCTATTTATTTATTTATTTGTTT	360
Db	8645		
		TGTCATTGCTCCCACATTCTGATGAGCAAACCGCTTCCCTATTTATTTATTTATTTGTTT	8704
QY	361	GTTTGTTTTGATTCAATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA	420
Db	8705		
		GTTTGTTTTGATTCAATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA	8764
QY	421	AAAGAGCCTAGTTTTTTAATAGCTATGGAAACAATTCAATTTGGA CTGGTGTGCTCTCTTT	480
Db	8765		
		AAAGAGCCTAGTTTTTTAATAGCTATGGAAACAATTCAATTTGGA CTGGTGTGCTCTCTTT	8824
QY	481	AAATCAAGTCCCTTTTAATTAACA CTGAAAAATATAAAGCTCAGATTTATTTAAATGGGAATA	540
Db	8825		
		AAATCAAGTCCCTTTTAATTAAGACTGAAAAATATAAAGCTCAGATTTATTTAAATGGGAATA	8884
QY	541	TTTATAAATGAGCAAAATATGATACTGTTTCAATGGTTC TGAATAAATAA ACTTCAC TGAAGAAA	600
Db	8885		
		TTTATAAATGAGCAAAATATCATACTGTTCAATGGTTC TGAATAAATAA ACTTCAC TGAAGAAA	8944

QY	601	AAAAAAAAGG	TCTCTCCTGATCAT	TGACTGTCTGGATTGACACTGACAGTAAGCAAAAC	660
Db	8945	AAAAAAAAGG	TCTCTCCTGATCAT	TGACTGTCTGGATTGACACTGACAGTAAGCAAAAC	90044
QY	661	AGGCTGTGAGAG	TTCTTTGGGACTAAGCCCACTCCTCAT	TGCTGAGTGCTGCAAGTACCTTA	720
Db	9005	AGGCTGTGAGAG	TTCTTTGGGACTAAGCCCACTCCTCAT	TGCTGAGTGCTGCAAGTACCTTA	90644
QY	721	GAAATATCCTT	GGCCACCGAAGACTATCCTCCTCACCCCATCCCCTTTATTTTCGTTGTTCA	780	
Db	9065	GAAATATCCTT	GGCCACCGAAGACTATCCTCCTCACCCCATCCCCTTTATTTTCGTTGTTCA	91244	
QY	781	ACAGAAGGATAT	TCAGTGCAACATCTGGAAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG	840	
Db	9125	ACAGAAGGATAT	TCAGTGCAACATCTGGAAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG	91844	
QY	841	GACTGGTAGTAA	CAGCTACCATGATTTATCTATCAATGCACCAAAACATCTGTTGAGCAAG	900	
Db	9185	GACTGGTAGTAA	CAGCTACCATGATTTATCTATCAATGCACCAAAACATCTGTTGAGCAAG	92444	
QY	901	CGCTATGTA	CTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCAACAAGTCCCTCCTCAGAT	960	
Db	9245	CGCTATGTA	CTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCAACAAGTCCCTCCTCAGAT	93044	
QY	961	AGGAGAGGCAG	CTAGTTATAAGCAGAAACAAGGTAACATGAC	1001	
Db	9305	AGGAGAGGCAG	CTAGTTATAAGCAGAAACAAGGTAACATGAC	9345	

RESULT 5

AAA50174

ID AAA50174 standard; DNA; 9721 BP.

AA AAA50174;

DT 07-NOV-2000 (first entry)

AA
DE
Human interleukin-1 beta allele 1 (+6912).

Interleukin-1 beta: IL-1B: human: polymorphism: inflammation: kw

coronary artery disease; osteoporosis; nephropathy; alopecia areata; KW

Graves disease; systemic lupus erythematosus; lichen sclerosus; KW

ulcerative colitis; diabetic retinopathy; periodontal disease; KW

KW juvenile chronic arthritis; psoriasis; insulin dependent diabetes;

KW asthma; lung fibrosis; chronic inflammatory liver disease;
KW

KW
KW
rheumatoid arthritis; chronic inflammatory lung disease;

antiinflammatory; osteopathic; dermatological; immunosuppressive; immunosuppressive;

[illegible]

antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
KW
v
v

XX
OS Homo sapiens.

XX	Key	Location/Qualifiers replace(8904,G)
FH		
FT	variation	

FT variation replace(8904,G)

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FT
/*tag= a

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FT /note= "IL-1B allele 1 (+6912)"

PN WO200047619-A1.

17-AUG-2000.

AA
PF 10-FEB-2000; 2000WO-US003443.

XX
PR 10-FEB-1999; 99US-00247874.

XX PA (INTE-) INTERLEUKIN GENETICS INC.

XX
PI
Duff GW. Di Giovine FS;

XX
DR WPI: 2000-558192/51.

PT Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin 1bsta, especially inflammatory

PT diseases.

XX PS Disclosure; Fig 1; 74pp; English.

XX CC The present sequence is that of human interleukin-1 beta (IL-1B) allele 1
CC (+6912), which is a form of the IL-1B gene that contains cytosine at
CC position +6912; IL-1B allele 2 (+6912) has guanine at this position (see
CC AAA50175). The invention is based on the identification of this novel
CC allele at marker +6912 of the IL-1B gene. The C to G transition occurs
CC within the 3' untranslated region of the IL-1B gene and results in an
CC increased level of IL-1B protein. Individuals homozygous for the IL-1B
CC allele 2 (+6912) accumulate approximately 4 times more immunoreactive IL-
CC 1B protein than homozygotes for IL-1B allele 1 (+6912). Methods and kits
CC are provided for detecting IL-1B allele 2 (+6912), or an allele in
CC linkage disequilibrium with an IL-1B allele 2 (+6912), and thereby
CC determining a patient's susceptibility to developing inflammatory
CC disorders, especially coronary artery disease, osteoporosis, nephropathy
CC in diabetes mellitus, alopecia areata, Graves disease, systemic lupus
CC erythematosus, lichen sclerosis, ulcerative colitis, diabetic
CC retinopathy, periodontal disease, juvenile chronic arthritis, psoriasis,
CC insulin dependent diabetes, asthma, chronic inflammatory liver disease,
CC chronic inflammatory lung disease, lung fibrosis, and rheumatoid
CC arthritis (claimed). Identification of the IL-1B allele 2 (+6912) and its
CC involvement in IL-1B overproduction also enables screening assays for
CC identifying IL-1B antagonists that can be used to treat conditions
CC associated with IL-1B allele 2 (+6912). Transgenic animals are also
CC claimed, and can be used to identify IL-1B agonists and antagonists, or
CC to confirm the safety and efficacy of candidate therapeutics

XX SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 3; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
DB |||||
DB 8345 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 8404
QY 61 AACAGAAAGGTTTGTAGTACGGCTATAGCCTGGACTTCTCTGTGTCTACACCAATGCC 120
DB |||||
DB 8405 AACAGAAAGGTTTGTAGTACGGCTATAGCCTGGACTTCTCTGTGTCTACACCAATGCC 8464
QY 121 CAACTGCCTGCTTAGGGTAGTGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
DB |||||
DB 8465 CAACTGCCTGCTTAGGGTAGTGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 8524
QY 181 CTCTCTCCTTTAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 240
DB |||||
DB 8525 CTCTCTCCTTTAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 8584
QY 241 CTACTCATTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 300
DB |||||
DB 8585 CTACTCATTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 8644
QY 301 TGTCATTCCGCTCCACATTCTGTATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
DB |||||
DB 8645 TGTCATTCCGCTCCACATTCTGTATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704
QY 361 GTTTGTGTTTGAATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 420
DB |||||
DB 8705 GTTTGTGTTTGAATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 8764
QY 421 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTT 480
DB |||||
DB 8765 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTT 8824
QY 481 AAATCAAGTCCTTTAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
DB |||||
DB 8825 AAATCAAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 8884
QY 541 TTTATAAATAGCAAAATATGATACCTGTTCAATGGTTCTGAAATAAACCCTCACTGAAGAA 600
DB |||||

DB 8885 TTTATAAATAGCAAAATATGATACCTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 8944
QY 601 AAAAAAAGGGTCTCTCTGATGATCATTTGACTGCTGGATTGACACTGACAGTAAGCAAAAC 660
DB |||||
DB 8945 AAAAAAAGGGTCTCTCTGATGATCATTTGACTGCTGGATTGACACTGACAGTAAGCAAAAC 9004
QY 661 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 720
DB |||||
DB 9005 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 9064
QY 721 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCCATCCCTTTATTTCTGTTGTTCA 780
DB |||||
DB 9065 GAAATATCTTGGCCACCGAAGACTATCTCTCTCAACCCATCCCTTTATTTCTGTTGTTCA 9124
QY 781 ACAGAAGGATATTTCAGTGCACATCTTGGAAACAGGATCAGCTGAAGCACTGCGAGGAGTCAG 840
DB |||||
DB 9125 ACAGAAGGATATTTCAGTGCACATCTTGGAAACAGGATCAGCTGAAGCACTGCGAGGAGTCAG 9184
QY 841 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 900
DB |||||
DB 9185 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 9244
QY 901 CGCTATGTACTAGGAGCTGGGACTACAGAGATGAGAACAGTCAACAGTCCCTCTCAGAT 960
DB |||||
DB 9245 CGCTATGTACTAGGAGCTGGGACTACAGAGATGAGAACAGTCAACAGTCCCTCTCAGAT 9304
QY 961 AGGAGAGGAGCTAGTTTATAAGCAGAAACAAGGTAACATGAC 1001
DB |||||
DB 9305 AGGAGAGGAGCTAGTTTATAAGCAGAAACAAGGTAACATGAC 9345

RESULT 6

AAF20945

ID AAF20945 standard; DNA; 9721 BP.

XX AC AAF20945;

XX AC AAF20945;

DT 14-MAR-2001 (first entry)

XX DE Human interleukin-1 polynucleotide fragment #2512.

XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

XX KW human; airway disorder; bronchoconstriction; lung inflammation;

XX KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

XX KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

XX KW respiratory obstruction; pulmonary obstruction; impeded respiration;

XX KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

XX KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

XX KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

XX KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

XX KW cancer; ss.

XX OS Homo sapiens.

XX XX WO200062736-A2.

PN 26-OCT-2000.

XX PF 24-MAR-2000; 2000WO-US008020.

XX PR 06-APR-1999; 99US-0127958P.

XX XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX PI Nyce JW;

XX XX WPI; 2000-679539/66.

DR Low adenosine (A) content antisense oligonucleotides which do not trigger

XX adenosine receptors during metabolism, useful e.g. for treating cancers

PT and respiratory obstructions.

PT XX

PS Claim 6; Fig 2; 102pp; English.

XX The present sequence is provided in a specification relating to a method for determining whether a subject has or is predisposed to develop an interstitial lung disease. The method involves detecting an interleukin-1 receptor antagonist (IL-1RN) (-2018) allele 2, a tumour necrosis alpha (TNF-A) (-308) allele 2, or an allele in linkage disequilibrium with either of these two alleles. The method may be used to determine whether a subject has or is predisposed to develop an interstitial pneumonia or a pulmonary fibrosis and other disorders such as rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, systemic sclerosis, dermatomyositis. The method is also used for identifying molecules which can be used as therapeutics for treating interstitial lung disease

SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match		99.7%;	Score 997.8;	DB 3;	Length 9721;
Best Local Similarity		99.8%;	Pred. No. 7.8e-235;		
Matches 999;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG	60		
DB	8345	GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG	8404		
QY	61	AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC	120		
DB	8405	AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC	8464		
QY	121	CAACTGCTGCCTTAGGGTAGTGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	180		
DB	8465	CAACTGCTGCCTTAGGGTAGTGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	8524		
QY	181	CTCTCTCTCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC	240		
DB	8525	CTCTCTCTCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC	8584		
QY	241	CTACTACTTAAAGCCCGCTGACAGAAACCAAGCCGACATTTGGTTCTAAGAAACCCCTC	300		
DB	8585	CTACTACTTAAAGCCCGCTGACAGAAACCAAGCCGACATTTGGTTCTAAGAAACCCCTC	8644		
QY	301	TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT	360		
DB	8645	TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT	8704		
QY	361	GTTTGTGTTTGAATTCATTTGTTGTTAATTTATTTCAAGGGGCAAGAGTACAGTGTCTGTA	420		
DB	8705	GTTTGTGTTTGAATTCATTTGTTGTTAATTTATTTCAAGGGGCAAGAGTACAGTGTCTGTA	8764		
QY	421	AAAGAGCCTAGTTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	480		
DB	8765	AAAGAGCCTAGTTTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	8824		
QY	481	AAATCAAGTCTCTTAAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	540		
DB	8825	AAATCAAGTCTCTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	8884		
QY	541	TTTATAAATGAGCAAAATATGATGTTCTGTTCAATGGTTCTGAAATAAATCACTGAGAAA	600		
DB	8885	TTTATAAATGAGCAAAATATGATGTTCTGTTCAATGGTTCTGAAATAAATCACTGAGAAA	8944		
QY	601	AAAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC	660		
DB	8945	AAAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC	9004		
QY	661	AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCATTTGCTGAGTGTGCAAGTACCTA	720		
DB	9005	AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCATTTGCTGAGTGTGCAAGTACCTA	9064		
QY	721	GAATATCTCTTGGCCACCGAGACTATCTCTCTCACCCATCCCTTTATTTCTGTTGTTCA	780		
DB	9065	GAATATCTCTTGGCCACCGAGACTATCTCTCTCACCCATCCCTTTATTTCTGTTGTTCA	9124		
QY	781	ACAGAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG	840		

DB	9125	ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG	9184		
QY	841	GACTGTACTAACAGACTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG	900		
DB	9185	GACTGTACTAACAGACTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG	9244		
QY	901	CGCTATGTACTAGGAGCTGGAGTACAGAGATGAGAACAGTCAAAAGTCCCTCCTCAGAT	960		
DB	9245	CGCTATGTACTAGGAGCTGGAGTACAGAGATGAGAACAGTCAAAAGTCCCTCCTCAGAT	9304		
QY	961	AGGAGAGGAGCTAGTTATTAAGCAGAAACAAGGTAACATGAC	1001		
DB	9305	AGGAGAGGAGCTAGTTATTAAGCAGAAACAAGGTAACATGAC	9345		

RESULT 8
AAC91434
ID AAC91434 standard; DNA; 9721 BP.

XX	AAC91434;
XX	20-MAR-2001 (first entry)
XX	Human IL-1B nucleotide sequence.
DE	Human; IL-1A; interleukin-1alpha; IL-1B; interleukin-1beta; IL-1RN;
XX	interleukin-1 receptor antagonist; vasotropic; antiinflammatory;
KW	hypotensive; anticoagulant; antilipemic; arterial restenosis;
KW	restenosis associated allele; RAA; occlusive cardiovascular disorder;
KW	restenosis detection; ds.
XX	Homo sapiens.
OS	WO200071753-A2.
XX	30-NOV-2000.
PD	24-MAY-2000; 2000WO-US014299.
XX	24-MAY-1999; 99US-00317674.
PR	01-NOV-1999; 99US-00431352.
XX	(INTE-) INTERLEUKIN GENETICS INC.
PA	Kornman KS, Duff GW, Crossman DC, Francis SE, Stephenson K;
XX	WPI; 2001-025173/03.

Diagnosing or determining susceptibility to developing restenosis involves detecting restenosis associated allele in a nucleic acid sample.

Disclosure; Fig 2; 129pp; English.
The present sequence is given in a specification relating to a method for determining whether a subject has or is predisposed to developing an arterial restenosis. The method comprises detecting a restenosis associated allele (RAA) in a nucleic acid sample from the subject, where detection of the RAA indicates that the subject has or is predisposed to the development of a restenosis. The restenosis associated allele pattern permits the diagnosis of occlusive cardiovascular disorder. The diagnosis allows the most suitable treatment methods for restenosis to be used e.g. selecting therapies for initial vascular stenosis most likely to avoid subsequent stenoses. The detection methods identify restenosis therapeutics, agonists and antagonists, (proteins, peptides, peptidomimetics, small molecules or nucleic acids, e.g. anti-sense, ribozyme and triplex nucleic acids) which are used to treat restenosis

Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 5; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
DB 8345 GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 8404
QY 61 AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTCTCTGTGTCTACACCAATGCC 120
DB 8405 AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTCTCTGTGTCTACACCAATGCC 8464
QY 121 CAACTGCTGCTCTAGGGTAGTGTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCTAG 180
DB 8465 CAACTGCTGCTCTAGGGTAGTGTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCTAG 8524
QY 181 CTCTCTCTCTCAGGGCCAAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 240
DB 8525 CTCTCTCTCTCAGGGCCAAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 8584
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCACGGCCACATTTGGTTCCTAAGAAACCCCTC 300
DB 8585 CTACTCACTTAAAGCCCGCTGACAGAAACCACGGCCACATTTGGTTCCTAAGAAACCCCTC 8644
QY 301 TGTCAATTCGCTCCACATCTCTGTATGAGCAACCGCTTCCCTATTATTTATTATTGTTT 360
DB 8645 TGTCAATTCGCTCCACATCTCTGTATGAGCAACCGCTTCCCTATTATTTATTATTGTTT 8704
QY 361 GTTTGTTTGAATTCATTGGTCTTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA 420
DB 8705 GTTTGTTTGAATTCATTGGTCTTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA 8764
QY 421 AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 480
DB 8765 AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT 8824
QY 481 AAATCAAGTCTCTTAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
DB 8825 AAATCAAGTCTCTTAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 8884
QY 541 TTTATAAATGAGCAAAATATGATCTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 600
DB 8885 TTTATAAATGAGCAAAATATGATCTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 8944
QY 601 AAAAAAAGGTCTCTCTGATCAATGACTGTCTGGATGACACTGACAGTAAGCAAAAC 660
DB 8945 AAAAAAAGGTCTCTCTGATCAATGACTGTCTGGATGACACTGACAGTAAGCAAAAC 9004
QY 661 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCCTCAATTTGCTGAGTGTGCAAGTACCTA 720
DB 9005 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCCTCAATTTGCTGAGTGTGCAAGTACCTA 9064
QY 721 GAAATATCCTTTGGCCACCGAAGACTATCTCTCCTCAACCCATCCCTTTATTTCTGTTGTTCA 780
DB 9065 GAAATATCCTTTGGCCACCGAAGACTATCTCTCCTCAACCCATCCCTTTATTTCTGTTGTTCA 9124
QY 781 ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCTAG 840
DB 9125 ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCTAG 9184
QY 841 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 900
DB 9185 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 9244
QY 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCAGAT 960
DB 9245 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCTCAGAT 9304
QY 961 AGGAGAGGCAGCTAGTTATAAGCAGAAACAGGTAAACATGAC 1001
DB 9305 AGGAGAGGCAGCTAGTTATAAGCAGAAACAGGTAAACATGAC 9345

RESULT 9
AAD35192
ID AAD35192 standard; DNA; 9721 BP.

XX AAD35192;
XX 25-JUL-2002 (first entry)
XX Human prointerleukin-1 beta (IL-1 beta) gene.
DE Unexplained recurrent pregnancy loss; immunologic reproductive failure;
XX URPL; prointerleukin-1beta; IL-1beta; human; ds.
KW Homo sapiens.
XX WO200222877-A2.
XX 21-MAR-2002.
XX 12-SEP-2001; 2001WO-US028465.
XX 12-SEP-2000; 2000US-0231785P.
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX (DAND) DANA FARBER CANCER INST INC.
XX Hill JA, Wang ZC, Anderson DJ, Yunis EJ;
XX WPI; 2002-362362/39.
DR Evaluating risk of unexplained recurrent pregnancy loss in a subject, by
XX testing presence of a variant in interleukin-1 beta promoter region
CC and/or in CD46 gene intron 1 region in a sample obtained from the
CC subject.
XX Example 2 and 3; Page 51-54; 57pp; English.
XX The invention relates to a method for evaluating and treating risk of
CC unexplained recurrent pregnancy loss (URPL) in a subject suspected of
CC having immunologic reproductive failure. The method involves testing a
CC sample obtained from the subject for the presence of a variant in the
CC human interleukin-1beta (IL-1beta) promoter region, and/or a variant in
CC the CD46 gene intron 1 region, where the presence of the variant,
CC indicates an elevated risk of developing recurrent pregnancy loss. The
CC present sequence is human prointerleukin-1 beta (IL-1 beta) gene
XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 6; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
DB 8345 GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 8404
QY 61 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTCTCTGTGTCTACACCAATGCC 120
DB 8405 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTCTCTGTGTCTACACCAATGCC 8464
QY 121 CAACTGCTGCTCTAGGGTAGTGTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCTAG 180
DB 8465 CAACTGCTGCTCTAGGGTAGTGTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCTAG 8524
QY 181 CTCTCTCTCTCAGGGCCAAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 240
DB 8525 CTCTCTCTCTCAGGGCCAAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 8584
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCACGGCCACATTTGGTTCCTAAGAAACCCCTC 300
DB 8585 CTACTCACTTAAAGCCCGCTGACAGAAACCACGGCCACATTTGGTTCCTAAGAAACCCCTC 8644
QY 301 TGTCAATTCGCTCCACATCTCTGTATGAGCAACCGCTTCCCTATTATTTATTATTGTTT 360
DB 8645 TGTCAATTCGCTCCACATCTCTGTATGAGCAACCGCTTCCCTATTATTTATTATTGTTT 8704

||||| 8825 AAATCAAGTCCTTTAATTAAAGCTGAAATATATAAAGCTCAGATTATTAAATGGAATA 8884
QY 541 TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 600
Db 8885 TTTATAAATGAGCAAAATATCACTACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 8944
QY 601 AAAAAAAAAAGGGTCTCTCTGATCATTTGACTGTCIGGATTGACACTGACAGTAAGCAAAAC 660
Db 8945 AAAAAAAAAAGGGTCTCTCTGATCATTTGACTGTCIGGATTGACACTGACAGTAAGCAAAAC 9004
QY 661 AGGCTGTGAGAGTTCTTGGGACTAAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 720
Db 9005 AGGCTGTGAGAGTTCTTGGGACTAAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 9064
QY 721 GAAATATCCTTGGCCACCGAAGACTATCCTCTCACCCATCCCTTTATTTCGTTGTTCA 780
Db 9065 GAAATATCCTTGGCCACCGAAGACTATCCTCTCACCCATCCCTTTATTTCGTTGTTCA 9124
QY 781 ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 840
Db 9125 ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 9184
QY 841 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAAACATCTGTTGAGCAAG 900
Db 9185 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAAACATCTGTTGAGCAAG 9244
QY 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCACAAGTCCCTCCTCAGAT 960
Db 9245 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCACAAGTCCCTCCTCAGAT 9304
QY 961 AGGAGGCGAGCTAGTTATAAGCAGAAACAAGGTAACATGAC 1001
Db 9305 AGGAGGCGAGCTAGTTATAAGCAGAAACAAGGTAACATGAC 9345

RESULT 11
AAD51464
ID AAD51464 standard; DNA; 9721 BP.
XX
AC AAD51464;
XX
DT 16-APR-2003 (first entry)
XX
DE Human interleukin-1B (IL-1B) gene.
XX
DE Drug screening; fungicide; gene therapy; antibacterial; infection;
KW virucide; human; interleukin-1; IL-1; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2002101015-A2.
XX
PD 19-DEC-2002.
XX
PF 11-JUN-2002; 2002WO-US018346.
XX
PR 11-JUN-2001; 2001US-0297305P.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Dower S, Duff GW;
XX
DR WPI; 2003-148793/14.
XX
PT New detection reagent, useful for monitoring molecular assembly events to
PT permit the dissection of genetic and non-genetic influences on biological
PT activity, comprises an interactive sensor pair.
XX
PS Disclosure; Fig 3; 56pp; English.
XX
CC The invention relates to methods, compositions and apparatus for
CC monitoring molecular assembly events. It also relates to a detection

CC reagent comprising an interactive sensor pair. The detection reagent is
CC useful for monitoring molecular assembly events to permit the dissection
CC of genetic and non-genetic influences on a particular biological
CC activity. The method is useful for linking genetic variations to
CC molecular and physiological events, drug screening, diagnostics, therapy
CC selection and dosing, patient monitoring or environmental safety. The
CC interactive sensor pairs may be used to screen for and identify novel
CC agonists and antagonists or other molecules that modulate a biological
CC activity. The method is also useful for selecting an appropriate targeted
CC therapeutic for a subject having an infection, including viral, bacterial
CC or fungal infection. It is also used in gene therapy. The present
CC sequence is human interleukin-1 (IL-1) allelic gene. This sequence is
CC used to illustrate the method of the invention
XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;
Query Match 99.7%; Score 997.8; DB 7; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGTACCCAGAGATCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
Db 8345 GCTGTACCCAGAGATCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 8404
QY 61 AACAGAAAAGTTTTGAGTACGGCTATAGCCTGGACCTTCTGTGTCTACACCAATGCC 120
Db 8405 AACAGAAAAGTTTTGAGTACGGCTATAGCCTGGACCTTCTGTGTCTACACCAATGCC 8464
QY 121 CAACTGCCTGCCTTAGGTTAGTACGGCTATAGCCTGGACCTTCTGTGTCTACACCAATGCC 180
Db 8465 CAACTGCCTGCCTTAGGTTAGTACGGCTATAGCCTGGACCTTCTGTGTCTACACCAATGCC 8524
QY 181 CTCTCTCCTTTACAGGGCCAATCCCGAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 240
Db 8525 CTCTCTCCTTTACAGGGCCAATCCCGAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 8584
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACACAGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db 8585 CTACTCACTTAAAGCCCGCTGACAGAAACACAGGCCACATTTGGTTCTAAGAAACCCCTC 8644
QY 301 TGTCACTTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db 8645 TGTCACTTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 8704
QY 361 GTTTGTTTGTGATTCATTGGTCTAATTATTATCAAGGGGGCAAGAGTAGCAGTGTCTGTA 420
Db 8705 GTTTGTTTGTGATTCATTGGTCTAATTATTATCAAGGGGGCAAGAGTAGCAGTGTCTGTA 8764
QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTCTTT 480
Db 8765 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTCTTT 8824
QY 481 AAATCAAGTCCTTTAATTAACACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATA 540
Db 8825 AAATCAAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATA 8884
QY 541 TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 600
Db 8885 TTTATAAATGAGCAAAATATCATCTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 8944
QY 601 AAAAAAAAAAGGGTCTCTCTGATCATTTGACTGTCIGGATTGACACTGACAGTAAGCAAAAC 660
Db 8945 AAAAAAAAAAGGGTCTCTCTGATCATTTGACTGTCIGGATTGACACTGACAGTAAGCAAAAC 9004
QY 661 AGGCTGTGAGAGTTCTTGGGACTAAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 720
Db 9005 AGGCTGTGAGAGTTCTTGGGACTAAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 9064
QY 721 GAAATATCCTTGGCCACCGAAGACTATCCTCTCACCCATCCCTTTATTTCGTTGTTCA 780
Db 9065 GAAATATCCTTGGCCACCGAAGACTATCCTCTCACCCATCCCTTTATTTCGTTGTTCA 9124
QY 781 ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 840

Db 9125 ACAGAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 9184
QY 841 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACACATCTGTTGAGCAAG 900
Db 9185 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACACATCTGTTGAGCAAG 9244
QY 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCCTCAGAT 960
Db 9245 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCCTCAGAT 9304
QY 961 AGGAGAGGCGAGCTAGTTATTAAGCAGCAACAAGGTAACATGAC 1001
Db 9305 AGGAGAGGCGAGCTAGTTATTAAGCAGCAACAAGGTAACATGAC 9345

RESULT 12
AAL54516
ID AAL54516 standard; DNA; 9721 BP.
XX
AC AAL54516;
XX
DT 16-APR-2003 (first entry)
XX
DE Interleukin-1B nucleotide sequence.
XX
KW Early onset; progression; ageing-related condition; EOA; allele;
interleukin; (IL)-1; pattern 1; pattern 2; pattern 3; osteoporosis;
osteoarthritis; wrinkled skin; age-related cancer; lifestyle; exercise;
diet; nutraceutical; ds.
XX
OS Unidentified.
XX
PN WO2002103031-A2.
XX
PD 27-DEC-2002.
XX
PF 17-JUN-2002; 2002WO-US019205.
XX
PR 15-JUN-2001; 2001US-0298493P.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Barnett K, Crossman DC, Duff GW, Francis SE, Kornman KS;
XX
DR WPI; 2003-167530/16.
XX
PT Determining a subject's susceptibility to an early onset or progression
of an aging-related condition, useful for customizing therapy, comprises
detecting the presence of an allele of an interleukin-1 pattern 1,
pattern 2 and/or pattern 3.
XX
PS Disclosure; Fig 5; 98pp; English.
XX

CC The invention relates to a novel method for determining a subject's
susceptibility to the early onset or progression of an ageing-related
condition (EOA). The novel method comprises assessing the subject's
genotype with respect to at least one allele of an interleukin (IL)-1
pattern 1, pattern 2 and/or pattern 3 (the presence or absence of at
least 1 allele provides information about the subject's susceptibility to
an early onset or progression of an ageing-related condition). The method
is useful for determining or predicting a subject's susceptibility to the
early onset or progression of an ageing-related condition (e.g.
osteoporosis, osteoarthritis, wrinkled skin, or age-related cancer) and
for determining an ageing-related phenotype. The method may be a
customised therapy based on the individual's genetic profile, to tailor a
recommended lifestyle, including changes in exercise and diet, and to
recommend nutraceuticals that are predicted to benefit a subject having a
particular IL-1 genotype and EOA predisposition. This polynucleotide
sequence represents an interleukin nucleotide sequence relating to the
invention
XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 7; Length 9721;
Best Local Similarity 99.8%; Pred. No. 7.8e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCAGAAAGGG 60
Db 8345 GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGCAGAAAGGG 8404
QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCCTGTTGTCTACACCAATGCC 120
Db 8405 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCCTGTTGTCTACACCAATGCC 8464
QY 121 CAACTGCCCTTAGGGTAGTGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
Db 8465 CAACTGCCCTTAGGGTAGTGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 8524
QY 181 CTCTCTCCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 240
Db 8525 CTCTCTCCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 8584
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCACATTTGGTTCCTAAGAAACCCCTC 300
Db 8585 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCACATTTGGTTCCTAAGAAACCCCTC 8644
QY 301 TGTCACTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT 360
Db 8645 TGTCACTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTT 8704
QY 361 GTTGTGTTTGAATTCATTTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA 420
Db 8705 GTTGTGTTTGAATTCATTTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA 8764
QY 421 AAAGAGCCTTAGTTTTTAATAGTATGGAATCAATCAATTTGGACTGGTGTCTCTCTTT 480
Db 8765 AAAGAGCCTTAGTTTTTAATAGTATGGAATCAATCAATTTGGACTGGTGTCTCTCTTT 8824
QY 481 AAATCAAGTCCTTTAATTAACACTGAAATATATAAGCTCAGATTATTATAAATGGGAATA 540
Db 8825 AAATCAAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTATAAATGGGAATA 8884
QY 541 TTTATAAATGAGCAAAATATGATACTGTTCAATGGTCTGAAATAAACTCACTGAAGAAA 600
Db 8885 TTTATAAATGAGCAAAATATGATACTGTTCAATGGTCTGAAATAAACTCACTGAAGAAA 8944
QY 601 AAAAAAAGGGTCTCTCTGATCATTTGACTGCTGGATTGACACTGACAGTAAGCAAAAC 660
Db 8945 AAAAAAAGGGTCTCTCTGATCATTTGACTGCTGGATTGACACTGACAGTAAGCAAAAC 9004
QY 661 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 720
Db 9005 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 9064
QY 721 GAAATATCCTTTGGCCACCGAAGACTATCCTCCTCACCCATCCCTTTATTTGTTTCA 780
Db 9065 GAAATATCCTTTGGCCACCGAAGACTATCCTCCTCACCCATCCCTTTATTTGTTTCA 9124
QY 781 ACAGAAGGATATTTCAGTGCACTCTGGAACAGGATCAGCTGAAGCACTGAGGGAGTCAG 840
Db 9125 ACAGAAGGATATTTCAGTGCACTCTGGAACAGGATCAGCTGAAGCACTGAGGGAGTCAG 9184
QY 841 GACTGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 900
Db 9185 GACTGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 9244
QY 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCCTCAGAT 960
Db 9245 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAACAAGTCCCTCCTCAGAT 9304
QY 961 AGGAGAGGCGAGCTAGTTATTAAGCAGCAACAAGGTAACATGAC 1001
Db 9305 AGGAGAGGCGAGCTAGTTATTAAGCAGCAACAAGGTAACATGAC 9345

RESULT 13
ACC83528
ID ACC83528 standard; DNA; 15402 BP.
XX
AC ACC83528;
XX
DT 08-SEP-2003 (first entry)
XX
DE Human interleukin-1 beta gene.
XX
KW Interleukin-1 beta; IL-1B; human; single nucleotide polymorphism; SNP;
KW antiinflammatory; nootropic; antirheumatic; antiarthritic; cardiant;
KW antiulcer; ophthalmological; antidiabetic; lipolytic; antiasthmatic;
KW gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(3870,t)
FT /*tag= a
FT /standard name= "Single nucleotide polymorphism"
FT /note= "-3737 polymorphic allele 1"
XX
PN WO2003044176-A2.
XX
PD 30-MAY-2003.
XX
PF 19-NOV-2002; 2002WO-US037222.
XX
PR 19-NOV-2001; 2001US-0331681P.
PR 05-JUN-2002; 2002US-0386020P.
XX
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Wyllie D, Duff GW, Aziz N, Hsieh CM;
XX
DR WPI; 2003-457608/43.
XX
PT New nucleic acid, useful for preparing a composition for treating an
PT inflammatory disease or condition associated with increased interleukin
PT production in a human subject, e.g. rheumatoid arthritis or ulcerative
PT colitis.
XX
PS Disclosure; Fig 1; 107pp; English.
XX
CC The present sequence is that of the interleukin-1 beta (IL-1B) gene
CC including the upstream promoter region. A novel function-altering
CC polymorphism has been discovered at position -3737 in the distal upstream
CC promoter region. The IL-1B (-3737) type 1 allele (C) is associated with
CC increased IL-1B expression and is associated with inflammatory disease. A
CC claimed method of diagnosing an increased likelihood of developing an
CC inflammatory disease or condition associated with increased interleukin
CC production in a subject involves determining the identity of the -3737 IL
CC -1B allele as a type 1 (C) or type 2 (T) promoter sequence. The
CC inflammatory disease is especially a periodontal disease or Alzheimer's
CC disease, or is amyotrophic lateral sclerosis, arthritis, collagen-induced
CC arthritis, juvenile chronic arthritis, juvenile rheumatoid arthritis,
CC osteoarthritis, asthma, cardiovascular disease, autoimmune diabetes,
CC insulin-dependent diabetes, diabetic periodontitis, diabetic retinopathy,
CC diabetic nephropathy, coeliac disease, chronic colitis, Crohn's disease,
CC inflammatory bowel disease, ulcerative colitis, gastric ulcer, hepatic
CC inflammation, cholesterol gallstones, hepatic fibrosis, Kawasaki's
CC syndrome, multiple sclerosis, nephropathy, neurodegenerative disease,
CC ophthalmopathy, pancreatic acinitis, pulmonary disease, restenosis,
CC rheumatoid arthritis, thyroiditis, alopecia areata, autoimmune
CC myocarditis and Graves' disease (all claimed). Determining the identity
CC of the -3737 IL-1B allele is also useful for determining whether a
CC subject can be effectively treated with a therapeutic drug
SQ Sequence 15402 BP; 4453 A; 3490 C; 3462 G; 3995 T; 0 U; 2 Other;

Query Match

99.7%; Score 997.8; DB 7; Length 15402;

RESULT 14

Best Local Similarity 99.8%; Pred. No. 9e-235;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
Db |||||
14026 GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 14085
QY 61 AACAGAAAGGTTTGTAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 120
Db |||||
14086 AACAGAAAGGTTTGTAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 14145
QY 121 CAACTGCCTGCCTTAGGGTAGTCTAAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
Db |||||
14146 CAACTGCCTGCCTTAGGGTAGTCTAAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 14205
QY 181 CTCTCTCCTTTTCAGGGCCAATCCCAGCCCTTTTGTGTGAGCCAGGCCCTCTCTCACCTCTC 240
Db |||||
14206 CTCTCTCCTTTTCAGGGCCAATCCCAGCCCTTTTGTGTGAGCCAGGCCCTCTCTCACCTCTC 14265
QY 241 CTACTCATTAAAGCCCGCTCGACAGAAACCCAGGCCACATTTGGTTCTTAAGAAACCCCTC 300
Db |||||
14266 CTACTCATTAAAGCCCGCTCGACAGAAACCCAGGCCACATTTGGTTCTTAAGAAACCCCTC 14325
QY 301 TGTCAATCGCTCCACATTCTGTATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db |||||
14326 TGTCAATCGCTCCACATTCTGTATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 14385
QY 361 GTTTGTTTGAATCATTGGTCTAATTATTCAAAGGGGGGCAAGTAGCAGTGTCTGTA 420
Db |||||
14386 GTTTGTTTGAATCATTGGTCTAATTATTCAAAGGGGGGCAAGTAGCAGTGTCTGTA 14445
QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTCTTT 480
Db |||||
14446 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTCTTT 14505
QY 481 AAATCAAGTCCTTAAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
Db |||||
14506 AAATCAAGTCCTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 14565
QY 541 TTTATAAATGAGCAAAATATGATACTGTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 600
Db |||||
14566 TTTATAAATGAGCAAAATATCATACTGTTCATGGTTCTGAAATAAACTTCACTGAAGAAA 14625
QY 601 AAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGATTGACACTGACAGTAAGCAAAAC 660
Db |||||
14626 AAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGATTGACACTGACAGTAAGCAAAAC 14685
QY 661 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 720
Db |||||
14686 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTTGCTGAGTGTGCAAGTACCTA 14745
QY 721 GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCTTTATTTCGTTGTTCA 780
Db |||||
14746 GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCATCCCTTTATTTCGTTGTTCA 14805
QY 781 ACAGAAAGGATATTTCAGTGCACATCTGGAAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 840
Db |||||
14806 ACAGAAAGGATATTTCAGTGCACATCTGGAAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG 14865
QY 841 GACTGGTAGTAACAGTACCATGATTATCTATCAATGCACCAACATCTGTTGAGCCAG 900
Db |||||
14866 GACTGGTAGTAACAGTACCATGATTATCTATCAATGCACCAACATCTGTTGAGCCAG 14925
QY 901 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCCTCAGAT 960
Db |||||
14926 CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCAAGTCCCTCCTCAGAT 14985
QY 961 AGGAGAGGCAGCTAGTTATAAGCAGAAACAGGTAACATGAC 1001
Db |||||
14986 AGGAGAGGCAGCTAGTTATAAGCAGAAACAGGTAACATGAC 15026

AAA34828
ID AAA34828 standard; DNA; 29433 BP.
XX
AC AAA34828;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2517.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 677-684; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytotatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
SQ Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 0 U; 2 Other;

Query Match 99.7%; Score 997.8; DB 3; Length 29433;
Best Local Similarity 99.8%; Pred. No. 1.1e-234;
Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 60
Db 21812 GCTGTACCCAGAGAGTCCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 21871
QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCCTGTTGTCTACCAATGCC 120
Db 21872 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTCCTGTTGTCTACCAATGCC 21931
QY 121 CAATGCTCCCTTAGGGTAGTCTTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db 21932 CAATGCTCCCTTAGGGTAGTCTTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 21991
QY 181 CTCTCTCTCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 240
Db 21992 CTCTCTCTCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 22051
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCACATTTGGTCTTAAGAAACCTC 300
Db 22052 CTACTCACTTAAAGCCCGCTGACAGAAACACCGGCACATTTGGTCTTAAGAAACCTC 22111
QY 301 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db 22112 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 22171
QY 361 GTTTGTTTTGATTCATTTGGTCTTAATTTAAAGGGGGCAAGAGTAGAGTGTCTGTA 420
Db 22172 GTTTGTTTTGATTCATTTGGTCTTAATTTAAAGGGGGCAAGAGTAGAGTGTCTGTA 22231
QY 421 AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTTGACTGGTGTCTCTCTTT 480
Db 22232 AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTTGACTGGTGTCTCTCTTT 22291
QY 481 AAATCAAGTCCTTTAAATTAACACTGAAATATATAAGCTCAGATTATTATAAATGGGAATA 540
Db 22292 AAATCAAGTCCTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTATAAATGGGAATA 22351
QY 541 TTTATAAATGAGCAAAATATGATGACTGTTCAATGGTCTTGAATAAATCACTGAAGAAA 600
Db 22352 TTTATAAATGAGCAAAATATGATGACTGTTCAATGGTCTTGAATAAATCACTGAAGAAA 22411
QY 601 AAAAAAAGGGTCTCTCTCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC 660
Db 22412 AAAAAAAGGGTCTCTCTCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAAC 22471
QY 661 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 720
Db 22472 AGGCTGTGAGAGTTCTTTGGGACTAAGCCCACTCTCTCATTTGCTGAGTGTGCAAGTACCTA 22531
QY 721 GAAATATCTTTGGCCACCGAAGACTATCTCTCTCACCCATCCCTTTATTTGTTTCA 780
Db 22532 GAAATATCTTTGGCCACCGAAGACTATCTCTCTCACCCATCCCTTTATTTGTTTCA 22591
QY 781 ACAGAGGATATTTCAGTGACATCTGGAACAGGATCAGCTGAAGCATGCGAGGAGTCAG 840
Db 22592 ACAGAGGATATTTCAGTGACATCTGGAACAGGATCAGCTGAAGCATGCGAGGAGTCAG 22651
QY 841 GACTGTAGTAACAGTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 900
Db 22652 GACTGTAGTAACAGTACCATGATTTATCTATCAATGCACCAACATCTGTTGAGCAAG 22711
QY 901 CGTATGTACTAGGAGCTGGAGTACAGAGATGAGAAACAGTCAAGTCCCTCTCAGAT 960
Db 22712 CGTATGTACTAGGAGCTGGAGTACAGAGATGAGAAACAGTCAAGTCCCTCTCAGAT 22771
QY 961 AGGAGAGGCGAGCTAGTTATAAGCAGAAACAAAGGTAACATGAC 1001
Db 22772 AGGAGAGGCGAGCTAGTTATAAGCAGAAACAAAGGTAACATGAC 22812

RESULT 15
AAF20950
ID AAF20950 standard; DNA; 29433 BP.
XX

AAF20950;
14-MAR-2001 (first entry)
Human interleukin-1 polynucleotide fragment #2517.
Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
human; airway disorder; bronchoconstriction; lung inflammation;
surfactant depletion; respiratory; bronchodilator; antiinflammatory;
immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
respiratory obstruction; pulmonary obstruction; impeded respiration;
surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
pulmonary hypertension; emphysema; pulmonary transplantation rejection;
chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
cancer; ss.
Homo sapiens.
WO200062736-A2.
26-OCT-2000.
24-MAR-2000; 2000WO-US008020.
06-APR-1999; 99US-0127958P.
(UYEC-) UNIV EAST CAROLINA.
(NYCE/) NYCE J W.
Nyce JW;
WPI; 2000-679539/66.
Low adenosine (A) content antisense oligonucleotides which do not trigger
adenosine receptors during metabolism, useful e.g. for treating cancers
and respiratory obstructions.
Disclosure; Page 221-227; 1592pp; English.
The present invention describes low adenosine (A) content antisense
oligonucleotides and compositions (I) comprising them. In the antisense
oligonucleotides the A is replaced by a 'Universal' or alternative base.
(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
The antisense oligonucleotides and (I) can be used to down-regulate the
expression and or activity of target polypeptides associated with
lung/respiratory disorders and malignancies, such as stimulating and
activating peptide factors and transmitters, transcription factors,
immunoglobulins and antibodies, antibody receptors, cytokines and
chemokines, endogenously produced specific and non-specific enzymes,
binding proteins, adhesion molecules and their receptors, cytokine and
chemokine receptors, adenosine receptors, bradykinin receptors, central
nervous system (CNS) and peripheral nervous and non-nervous system
receptors, CNS and peripheral nervous and non-nervous system peptide
transmitters, defensins, growth factors, vasoactive peptides and
receptors, binding proteins and malignancy associated proteins. The
antisense oligonucleotides may be used in this way to treat disorders
including respiratory obstruction (especially pulmonary obstruction
and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
surfactant hypoproduction which are associated with a disease or
condition selected from pulmonary vasoconstriction, inflammation,
allergies, asthma, impeded respiration, respiratory distress syndrome
(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
pulmonary transplantation rejection, pulmonary infections, bronchitis,
and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
fragments and antisense oligonucleotides used in the exemplification of
the present invention

Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 0 U; 2 Other;

Query Match

99.7%; Score 997.8; DB 3; Length 29433;

Search completed: July 2, 2004, 11:27:15

Best Local Similarity 99.8%; Pred. No. 1.1e-234; Matches 999; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	60
Db	21812	GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	21871
QY	61	AACAGAAAGGTTTTTGTAGTACGGCTATAGCTGGAGCTTTTCTGTGTCTACACCAATGCC	120
Db	21872	AACAGAAAGGTTTTTGTAGTACGGCTATAGCTGGAGCTTTTCTGTGTCTACACCAATGCC	21931
QY	121	CAACTGCTGCTTCTAGGTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG	180
Db	21932	CAACTGCTGCTTCTAGGTAGTCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG	21991
QY	181	CTCTCTCTCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC	240
Db	21992	CTCTCTCTCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC	22051
QY	241	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCGACATTTGGTTCTAAGAAACCCCTC	300
Db	22052	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCGACATTTGGTTCTAAGAAACCCCTC	22111
QY	301	TGTCATTGCTCCACATTCCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT	360
Db	22112	TGTCATTGCTCCACATTCCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT	22171
QY	361	GTTTTGTTTGATTTCATTGGTCTTAATTTATTCAAAGSGGCAAGTAGCAGTGTCTGTA	420
Db	22172	GTTTTGTTTGATTTCATTGGTCTTAATTTATTCAAAGSGGCAAGTAGCAGTGTCTGTA	22231
QY	421	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT	480
Db	22232	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT	22291
QY	481	AAATCAAGTCTTTAATTAACACTGAAAAATATATAAGCTCAGATTATTTAAATGGGAATA	540
Db	22292	AAATCAAGTCTTTAATTAAGACTGAAAAATATATAAGCTCAGATTATTTAAATGGGAATA	22351
QY	541	TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAATCTCACTGAAGAAA	600
Db	22352	TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAATCTCACTGAAGAAA	22411
QY	601	AAAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGAATTGACACTGACAGTAAGCAAAAC	660
Db	22412	AAAAAAAAGGGTCTCTCTGATCATTTGACTGTCTGGAATTGACACTGACAGTAAGCAAAAC	22471
QY	661	AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCTCATTCCTGAGTGTGCAAGTACCTA	720
Db	22472	AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCTCTCATTCCTGAGTGTGCAAGTACCTA	22531
QY	721	GAAATATCCTTGGCCACCGAAGACTATCTCTCCTCACCCATCCCTTTATTTTCGTTGTTCA	780
Db	22532	GAAATATCCTTGGCCACCGAAGACTATCTCTCCTCACCCATCCCTTTATTTTCGTTGTTCA	22591
QY	781	ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG	840
Db	22592	ACAGAAGGATATTTCAGTGCACATCTGGAACAGGATCAGCTGAAGCACTGCAGGGAGTCAG	22651
QY	841	GACTGGTAGTAACAGCTACCATGATTATCTATCAATGCACCAAAACATCTGTTGAGCAAG	900
Db	22652	GACTGGTAGTAACAGCTACCATGATTATCTATCAATGCACCAAAACATCTGTTGAGCAAG	22711
QY	901	CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCACAAGTCCCTCCTCAGAT	960
Db	22712	CGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAAACAGTCACAAGTCCCTCCTCAGAT	22771
QY	961	AGGAGAGGCAGCTAGTTATTAAGCAGAACAAAGGTAACATGAC	1001
Db	22772	AGGAGAGGCAGCTAGTTATTAAGCAGAACAAAGGTAACATGAC	22812

Tue Jul 6 08:49:57 2004

us-09-247-874e-2_copy_8345_9345.rng

Page 16

Job time : 467 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 10:39:01 ; Search time 2592 Seconds
(without alignments)
11532.424 Million cell updates/sec

Title: US-09-247-874E-2_COPY_8345_9345
Perfect score: 1001
Sequence: 1 gctgtaccagagagtcctg.....gcagacaaggtacatgac 1001

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	595.4	59.5	705	13	BU626628
C 2	595.4	59.5	777	14	CD367424
C 3	593.8	59.3	618	14	CD368885
C 4	593.8	59.3	618	14	CD370914

C 5	593.8	59.3	668	14	CA431510	UI-H-FT0-
C 6	593.8	59.3	671	14	CA307004	UI-H-FT1-
C 7	593.8	59.3	701	13	BU626429	UI-H-FT0-
C 8	593.8	59.3	704	13	BU626613	UI-H-FT0-
C 9	593.8	59.3	706	13	BU626909	UI-H-FT0-
C 10	593.8	59.3	767	14	CA305984	UI-H-FT1-
C 11	593.8	59.3	767	14	CA442834	UI-H-DP0-
C 12	593.8	59.3	770	12	BQ000281	UI-H-DP0-
C 13	593.8	59.3	777	14	CA431534	UI-H-FT0-
C 14	593.8	59.3	798	14	CA307234	UI-H-FT1-
C 15	592.8	59.2	703	12	BQ001221	UI-H-DH1-
C 16	592.2	59.2	665	14	CD367786	UI-H-FT1-
C 17	592.2	59.2	704	14	CA443067	UI-H-DP0-
C 18	589.6	58.9	669	13	BU626499	UI-H-FT0-
C 19	588.4	58.8	638	13	BU626893	UI-H-FT0-
C 20	585.8	58.5	603	14	CD370521	UI-H-FT1-
C 21	579.8	57.9	793	12	BM999417	UI-H-DP0-
C 22	577.6	57.7	817	9	AI609005	tw85g07.x
C 23	573.8	57.3	656	14	CA310014	UI-H-FT1-
C 24	573.8	57.3	696	13	BU626962	UI-H-FT0-
C 25	567.4	56.7	619	14	CA441158	UI-H-DP0-
C 26	567.2	56.7	673	13	BU626793	UI-H-FT0-
C 27	562	56.1	618	10	AW273081	xu27h01.x
C 28	554.2	55.4	575	14	CA431636	UI-H-FT0-
C 29	543	54.2	749	12	BG117168	602346446
C 30	539.2	53.9	911	12	BG194765	BG194765 RST14064
C 31	536.8	53.6	698	9	AI471571	AI471571 t198h09.x
C 32	536	53.5	676	14	CA310223	CA310223 UI-H-FT1-
C 33	523	52.2	548	12	BM997237	UI-H-DH0-
C 34	506.2	50.6	554	9	AA577318	nm89a08.s
C 35	502	50.1	521	9	AI022364	ow64g05.x
C 36	481.6	48.1	549	9	AI566931	tq67h02.x
C 37	461.8	46.1	528	9	AI678441	tu82d01.x
C 38	437.6	43.7	514	9	AA131744	zl35f02.s
C 39	430	43.0	746	12	BI519707	BI519707 603061928
C 40	400	40.0	454	14	D20737	HUMGS01714
C 41	399.6	39.9	430	14	W47101	W47101 zc39b04.s1
C 42	389.8	38.9	703	9	AV715551	AV715551 AV715551
C 43	388	38.8	413	14	W38319	W38319 zc77b02.s1
C 44	384	38.4	429	14	T29172	EST1708 Hu
C 45	357.6	35.7	741	14	CD639977	CD639977 AGENCOURT

ALIGNMENTS

RESULT 1
BU626628/c
LOCUS
DEFINITION
UI-H-FT0-bhm-1-22-0-UI.s1 NCI CGAP_FTO Homo sapiens cDNA clone
UI-H-FT0-bhm-1-22-0-UI 3', mRNA sequence.
705 bp mRNA linear EST 23-SEP-2002
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BU626628
UI-H-FT0-bhm-1-22-0-UI.s1 NCI CGAP_FTO Homo sapiens cDNA clone
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COMMENT

BU626628
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UI-H-FT0-bhm-1-22-0-UI 3', mRNA sequence.
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TITLE
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UI-H-FT0-bhm-1-22-0-UI 3', mRNA sequence.
705 bp mRNA linear EST 23-SEP-2002
ACCESSION
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SOURCE
ORGANISM
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AUTHORS
TITLE

Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
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/clone_lib="NCI CGAP FT0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_FT0 is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 59.5%; Score 595.4; DB 13; Length 705;
Best Local Similarity 99.7%; Pred. No. 3.2e-108;
Matches 607; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACACCAATGCC 120
Db 551 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCTGGACTTTTCTGTGTCTACACCAATGCC 492
QY 121 CAATGCGCTGCTTAGGGTAGTGCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db 491 CAATGCGCTGCTTAGGGTAGTGCTAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 432
QY 181 CTCTCTCTCTTTCAGGGCCATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC 240
Db 431 CTCTCTCTCTTTCAGGGCCATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC 372
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QY 361 GTTTGTTTGTATTCATTCGTTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA 420
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RESULT 2

CD367424/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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UI-H-FT1-bjr-k-07-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bjr-k-07-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 777)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 59.5%; Score 595.4; DB 14; Length 777;
Best Local Similarity 99.7%; Pred. No. 3.1e-108;
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QY 1 GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGAGTCAATCCCTAGGCTGGCAGAAAGG 60
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QY 121 CAACCTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCTAG 180
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Db 132 AAATCAAGTCTTTAAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 73

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Db 12 AAAAAAAAA 4
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-r@mail.nih.gov
  Tissue Procurement: Dr. Gary W. Hunninghake, U of I
  CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/cgap.html
  The following repetitive elements were found in this cDNA
  sequence: 221-272, >(TAAA)n#Simple_repeat
  Seq primer: M13 FORWARD
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      NCI_CGAP_Ft1 is a normalized cDNA library constructed from
      a pool of 81 RNA samples from Alveolar Macrophages
      challenged with different treatments. The library was
      normalized according to Bonaldo, Lennon and Soares, Genome
      Research, 6:791-806, 1996. First strand cDNA synthesis was
      primed with an oligo-dT primer containing a Not I site.
      Double stranded cDNA was ligated to an EcoR I adaptor,
      digested with Not I, and cloned directionally into
      pT73-Pac vector. The oligonucleotide used to prime the
      synthesis of first-strand cDNA contains a library tag
      sequence that is located between the Not I site and the
      (dT)18 tail. The sequence tag for this library is
      GGCCATGCCG. The tissue was provided by Dr. Gary W.
      Hunninghake of the University of Iowa.
      TAG_TISSUE=Human Lung Alveolar Macrophage
      TAG_LIB=UI-H-FT1
      TAG_SEQ=GGCCATGCCG"
ORIGIN
  *Query Match 59.3%; Score 593.8; DB 14; Length 618;
  Best Local Similarity 99.5%; Pred.No. 7.1e-108;
  Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGTCTCTGTGCTGAATGTGAGTCAATCCCTAGGCTGGCAGAAAGG 60
Db 611 GCTGTACCCAGAGTCTCTGTGCTGAATGTGAGTCAATCCCTAGGCTGGCAGAAAGG 552

QY 61 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTTCCGTGTGTACACCAATGCC 120
Db 551 AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGGACTTTTCCGTGTGTACACCAATGCC 492

QY 121 CAACCTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCTAG 180
Db 491 CAACCTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCTAG 432

QY 181 CTCTCTCTCTTTCAGGGCCCAATCCCAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 240
Db 431 CTCTCTCTCTTTCAGGGCCCAATCCCAGCCCTTTTGTGTAGCCAGGCTCTCTCACCTCTC 372

QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTTCTAAGAAACCCCTC 312

QY 301 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTTATTTATTTGTTT 360
Db 311 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTTATTTATTTGTTT 252

QY 361 GTTTGTTTGTATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA 420
Db 251 GTTTGTTTGTATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTA 193

QY 421 AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTCAAATTTGGACTGGTGTCTCTCTT 480
Db 192 AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTCAAATTTGGACTGGTGTCTCTCTT 133

QY 481 AAATCAAGTCTTTAAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
Db 132 AAATCAAGTCTTTAAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGGAATA 73

QY 541 TTTATAAATGAGCAAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAA 600
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Db      72 TTTATAAATGAGCAATATCATACTGTTCAATGGTCTGGAATAAAGCTTCACTGAAGAAA 13
QY      601 AAAAAAAAAA 609
Db      12 AAAAAAAAAA 4

RESULT 4
CD370914/c
LOCUS
DEFINITION
  UI-H-FT1-bjz-j-02-0-UI.s1 NCI_CGAP_FTI Homo sapiens cDNA clone
  UI-H-FT1-bjz-j-02-0-UI 3', mRNA sequence.
ACCESSION
  CD370914
VERSION
  CD370914.1 GI:31155004
KEYWORDS
  EST.
SOURCE
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ORGANISM
  Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 618)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Dr. Gary W. Hunninghake, U of I
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/cgap.html
  The following repetitive elements were found in this cDNA
  sequence: 221-272, >(TAAA)n#Simple_repeat
  Seq primer: M13 FORWARD
  POLYA=Yes.
FEATURES
  source
  1..618
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="UI-H-FT1-bjz-j-02-0-UI"
  /tissue_type="Aveolar Macrophage"
  /dev_stage="Adult"
  /lab_host="DH10B (Life Technologies)"
  /clone_lib="NCI_CGAP_FTI"
  /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
  modified polylinker; Site 1: EcoR I; Site 2: Not I;
  NCI_CGAP_FTI is a normalized cDNA library constructed from
  a pool of 81 RNA samples from Alveolar Macrophages
  challenged with different treatments. The library was
  normalized according to Bonaldo, Lennon and Soares, Genome
  Research, 6:791-806, 1996. First strand cDNA synthesis was
  primed with an oligo-dT primer containing a Not I site.
  Double stranded cDNA was ligated to an EcoR I adaptor,
  digested with Not I, and cloned directionally into
  pT7T3-Pac vector. The oligonucleotide used to prime the
  synthesis of first-strand cDNA contains a library tag
  sequence that is located between the Not I site and the
  (dT)18 tail. The sequence tag for this library is
  GGCCATGCCG. The tissue was provided by Dr. Gary W.
  Hunninghake of the University of Iowa.
  TAG_TISSUE=Human Lung Aveolar Macrophage
  TAG_LIB=UI-H-FT1
  TAG_SEQ=GGCCATGCCG"
ORIGIN
  Query Match 59.3%; Score 593.8; DB 14; Length 618;
  Best Local Similarity 99.5%; Pred. No. 7.1e-108;
  Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
  QY 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
```

```
Db      611 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 552
QY      61 AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTCTCTGTGTGTCTACCAATGCC 120
Db      551 AACAGAAAGGTTTTGAGTACGGCTATAGCCTGGACTTCTCTGTGTGTCTACCAATGCC 492
QY      121 CAACTGCCTTCTAGGGTAGTGTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db      491 CAACTGCCTTCTAGGGTAGTGTAAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 432
QY      181 CTCTCTCTTTTCAAGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 240
Db      431 CTCTCTCTTTTCAAGGCCCAATCCCGAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 372
QY      241 CTACTCACTTAAAGCCCGCTTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db      371 CTACTCACTTAAAGCCCGCTTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCCTC 312
QY      301 TGTCACTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db      311 TGTCACTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 252
QY      361 GTTTGTTTTCATTCATTGGTCTAATTATTCAAAGSGGGCAAGAAGTAGCAGTGTCTGTA 420
Db      251 GTTTGTTTTCATTCATTGGTCTAATTATTCAAAGSGGGCAAGAAGTAGCAGTGTCTGTA 193
QY      421 AAAGAGCCTAGTTTTTAAATAGTATGGAATCAATCAATTTGGACTGGTGTGCTCTCTTT 480
Db      192 AAAGAGCCTAGTTTTTAAATAGTATGGAATCAATCAATTTGGACTGGTGTGCTCTCTTT 133
QY      481 AAATCAAGTCTCTTTAAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 540
Db      132 AAATCAAGTCTCTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 73
QY      541 TTTATAAATGAGCAAAATATGATACTGTTCAATGGTCTGAAATAAACTCACTGAAGAAA 600
Db      72 TTTATAAATGAGCAAAATATGATACTGTTCAATGGTCTGAAATAAACTCACTGAAGAAA 13
QY      601 AAAAAAAAAA 609
Db      12 AAAAAAAAAA 4

RESULT 5
CA431510/c
LOCUS
DEFINITION
  UI-H-FT0-bhm-i-17-0-UI.s1 NCI_CGAP_FTO Homo sapiens cDNA clone
  UI-H-FT0-bhm-i-17-0-UI 3', mRNA sequence.
ACCESSION
  CA431510
VERSION
  CA431510.1 GI:24794230
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 668)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Robeff-Pamela, U of I
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@uiowa.edu
  The following repetitive elements were found in this cDNA
  sequence: 221-272, >(TAAA)n#Simple_repeat
  Seq primer: M13 FORWARD
  POLYA=Yes.
  CA431510 668 bp mRNA linear EST 07-NOV-2002
  UI-H-FT0-bhm-i-17-0-UI.s1 NCI_CGAP_FTO Homo sapiens cDNA clone
  UI-H-FT0-bhm-i-17-0-UI 3', mRNA sequence.
  CA431510
  CA431510.1 GI:24794230
  EST.
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 668)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Robeff-Pamela, U of I
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@uiowa.edu
  The following repetitive elements were found in this cDNA
  sequence: 221-272, >(TAAA)n#Simple_repeat
  Seq primer: M13 FORWARD
  POLYA=Yes.
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FEATURES source Location/Qualifiers 1. .668 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-H-FT0-bhm-i-17-0-UI" /tissue_type="Alveolar Macrophage" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI_CGAP_FT0" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FT0 is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dTr)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa. TAG_TISSUE=Human Lung Aveolar Macrophage TAG_LIB=UI-H-FT0 TAG_SEQ=GGCCATGCCG

ORIGIN Query Match 59.3%; Score 593.8; DB 14; Length 668; Best Local Similarity 99.5%; Pred. No. 6.8e-108; Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 60
Db |||
QY 61 AACAGAAAGGTTTTTGTAGTACGCTATAGCCCTGGACTTCCTGTTGTCTACACCAATGCC 120
Db |||
QY 551 AACAGAAAGGTTTTTGTAGTACGCTATAGCCCTGGACTTCCTGTTGTCTACACCAATGCC 492
Db |||
QY 121 CAACTGCCTGCCTTAGGGTAGTGTGAAGAGGATCTCTCTCCATCAGCCAGGACAGTCAG 180
Db |||
QY 491 CAACTGCCTGCCTTAGGGTAGTGTGAAGAGGATCTCTCTCCATCAGCCAGGACAGTCAG 432
QY 181 CTCTCTCCTTTACAGGGCCCAATCCCAGGCCCTTTTGTGTAGCCAGGCCCTCTCTACCTCTC 240
Db |||
QY 431 CTCTCTCCTTTACAGGGCCCAATCCCAGGCCCTTTTGTGTAGCCAGGCCCTCTCTACCTCTC 372
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCAACCGGCACATTTGGTTCTAAGAAACCCCTC 300
Db |||
QY 371 CTACTCACTTAAAGCCCGCTGACAGAAACCAACCGGCACATTTGGTTCTAAGAAACCCCTC 312
QY 301 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCTATTTATTTATTTGTTT 360
Db |||
QY 311 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCTATTTATTTATTTGTTT 252
QY 361 GTTTGTTTTCATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCTGTCTGTA 420
Db |||
QY 251 GTTTGTTT-ATTCAATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCTGTCTGTA 193
QY 421 AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGGCTCTCTTT 480
Db |||
QY 192 AAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGGCTCTCTTT 133
QY 481 AAATCAAGTCCTTTAATTAACACTGAAATAATATAAGCTCAGATTATTTAATGGGAATA 540
Db |||
QY 132 AAATCAAGTCCTTTAATTAAGACTGAAATAATATAAGCTCAGATTATTTAATGGGAATA 73
QY 541 TTTATAATGACAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 600
Db |||

Db 72 TTTATAAATGAGCAAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 13

QY 601 AAAAAAAAA 609
Db 12 AAAAAAAAA 4

RESULT 6 CA307004 671 bp mRNA linear EST 01-NOV-2002
CA307004/c UI-H-FT1-bhu-c-24-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
LOCUS UI-H-FT1-bhu-c-24-0-UI 3', mRNA sequence.
DEFINITION CA307004
ACCESSION CA307004.1 GI:24470058
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 671)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers 1. .671 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-H-FT1-bhu-c-24-0-UI" /tissue_type="Alveolar Macrophage" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI_CGAP_FT1" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dTr)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG_TISSUE=Human Lung Aveolar Macrophage TAG_LIB=UI-H-FT1 TAG_SEQ=GGCCATGCCG

ORIGIN Query Match 59.3%; Score 593.8; DB 14; Length 671; Best Local Similarity 99.5%; Pred. No. 6.8e-108; Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGGG 60
Db |||

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Db 611 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 552
QY 61 AACAGAAAGGTTTGTAGTACGGCTATAGCTGAGCTTCTCTGTGTCTACACCAATGCC 120
Db 551 AACAGAAAGGTTTGTAGTACGGCTATAGCTGAGCTTCTCTGTGTCTACACCAATGCC 492
QY 121 CAACTGCCTCCCTTAGGGTAGTGAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db 491 CAACTGCCTCCCTTAGGGTAGTGAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 432
QY 181 CTCTCTCCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 240
Db 431 CTCTCTCCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 372
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCCACATTTGGTTCTAAGAAACCCCTC 312
QY 301 TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTGTTT 360
Db 311 TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTGTTT 252
QY 361 GTTTGTTTGTATTCATTTGCTTAATTTATTTCAAGGGGCAAGAGTAGCAGTGTCTGTA 420
Db 251 GTTTGTTTGTATTCATTTGCTTAATTTATTTCAAGGGGCAAGAGTAGCAGTGTCTGTA 193
QY 421 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTAAGCTCAGATTTATTTAAATGGGAATA 540
Db 192 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTAAGCTCAGATTTATTTAAATGGGAATA 73
QY 541 TTTATAATGAGCAAAATATGATAGTGTTCATGTTTCTGAAATAAACCTCACTGAAGAAA 600
Db 72 TTTATAATGAGCAAAATATGATAGTGTTCATGTTTCTGAAATAAACCTCACTGAAGAAA 13
QY 601 AAAAAAAAA 609
Db 12 AAAAAAAAA 4
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BU626429/c
LOCUS
DEFINITION
UI-H-FT0-bhm-g-02-0-UI.s1 NCI CGAP_FTO Homo sapiens cDNA clone
UI-H-FT0-bhm-g-02-0-UI 3', mRNA sequence.
ACCESSION
BU626429
VERSION
BU626429.1 GI:23292644
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT0-bhm-g-02-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FTO"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_FTO is a cDNA library constructed from a pool of
81 RNA samples from Alveolar Macrophages challenged with
different treatments. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GGCCATGCCG. The cell line
was provided by Gary W. Hunninghake from the University of
Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"
ORIGIN
```

```
Query Match 59.3%; Score 593.8; DB 13; Length 701;
Best Local Similarity 99.5%; Pred. No. 6.7e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 60
Db 611 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG 552
QY 61 AACAGAAAGGTTTGTAGTACGGCTATAGCCCTGGACTTCTCTGTGTCTACACCAATGCC 120
Db 551 AACAGAAAGGTTTGTAGTACGGCTATAGCCCTGGACTTCTCTGTGTCTACACCAATGCC 492
QY 121 CAACTGCCTCCCTTAGGGTAGTGAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db 491 CAACTGCCTCCCTTAGGGTAGTGAAGAGGATCTCTGTCCATCAGCCAGGACAGTCAG 432
QY 181 CTCTCTCCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 240
Db 431 CTCTCTCCTTTCAGGGCCAAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 372
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCCACATTTGGTTCTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCCACATTTGGTTCTAAGAAACCCCTC 312
QY 301 TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTGTTT 360
Db 311 TGTCATTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTTATTTATTTGTTT 252
QY 361 GTTTGTTTGTATTCATTTGCTTAATTTATTTCAAGGGGCAAGAGTAGCAGTGTCTGTA 420
Db 251 GTTTGTTTGTATTCATTTGCTTAATTTATTTCAAGGGGCAAGAGTAGCAGTGTCTGTA 193
QY 421 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTAAGCTCAGATTTATTTAAATGGGAATA 480
Db 192 AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTAAGCTCAGATTTATTTAAATGGGAATA 133
QY 481 AAATCAAGTCTTTTAAATTAACACTGAAATATATAAGCTCAGATTTATTTAAATGGGAATA 540
Db 132 AAATCAAGTCTTTTAAATTAACACTGAAATATATAAGCTCAGATTTATTTAAATGGGAATA 73
QY 541 TTTATAAATGAGCAAAATATGATAGTGTTCATGTTTCTGAAATAAACCTCACTGAAGAAA 600
Db 72 TTTATAAATGAGCAAAATATGATAGTGTTCATGTTTCTGAAATAAACCTCACTGAAGAAA 13
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QY 601 AAAAAAAAAA 609
Db 12 AAAAAAAAAA 4

RESULT 8
BU626613/c
LOCUS
DEFINITION
UI-H-FT0-bhm-j-10-0-UI.s1 NCI_CGAP_FT0 Homo sapiens cDNA clone
UI-H-FT0-bhm-j-10-0-UI 3', mRNA sequence.
ACCESSION
BU626613
VERSION
GI:23292828
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 704)
REFERENCE
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..704
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT0-bhm-j-10-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_FT0 is a cDNA library constructed from a pool of
81 RNA samples from Alveolar Macrophages challenged with
different treatments. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GGCCATGCCG. The cell line
was provided by Gary W. Hunninghake from the University of
Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 59.3%; Score 593.8; DB 13; Length 704;
Best Local Similarity 99.5%; Pred.No. 6.6e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
Db 611 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 552

QY 61 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 120
Db 551 AACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 492

QY 121 CAACCTGCCTCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
Db 491 CAACCTGCCTCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 432

QY 181 CTCTCTCCTTTTCAGGGCCCAATCCCGCAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 240
Db 431 CTCTCTCCTTTTCAGGGCCCAATCCCGCAGCCCTTTTGTGTAGCCAGGCCCTCTCTCACCTCTC 372

QY 241 CTACTCACTTAAAGCCCGCCTGACAGAAACCCAGGCCACATTTGGTTCTTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCCTGACAGAAACCCAGGCCACATTTGGTTCTTAAGAAACCCCTC 312

QY 301 TGTCACTTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db 311 TGTCACTTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 252

QY 361 GTTTGTTTGTATTCAATTGGTCTAAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA 420
Db 251 GTTTGTTT-ATTCAATTGGTCTAAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA 193

QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTT 480
Db 192 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTT 133

QY 481 AAATCAAGTCCTTTAATTAACACTGAAATATATATAGCTCAGATTATTATAATGGGAATA 540
Db 132 AAATCAAGTCCTTTAATTAAGACTGAAATATATATAGCTCAGATTATTATAATGGGAATA 73

QY 541 TTTATAAATGAGCAAAATATGATACTGTTCATTTCAATGGTTCTGAAATAAAGTTCACTGAAGAAA 600
Db 72 TTTATAAATGAGCAAAATATCATACTGTTCATTTCAATGGTTCTGAAATAAAGTTCACTGAAGAAA 13

QY 601 AAAAAAAAAA 609
Db 12 AAAAAAAAAA 4

RESULT 9
BU626909/c
LOCUS
DEFINITION
UI-H-FT0-bhm-h-03-0-UI.s1 NCI_CGAP_FT0 Homo sapiens cDNA clone
UI-H-FT0-bhm-h-03-0-UI 3', mRNA sequence.
ACCESSION
BU626909
VERSION
GI:23293124
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 706)
REFERENCE
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
1..706
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT0-bhm-h-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_FT0 is a cDNA library constructed from a pool of
81 RNA samples from Alveolar Macrophages challenged with
different treatments. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GGCCATGCCG. The cell line
was provided by Gary W. Hunninghake from the University of
Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 59.3%; Score 593.8; DB 13; Length 704;
Best Local Similarity 99.5%; Pred.No. 6.6e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
Db 611 GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 552

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT0-bhn-h-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT0 is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I adaptor. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 59.3%; Score 593.8; DB 13; Length 706;
Best Local Similarity 99.5%; Pred. No. 6.6e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
Db |||||
611 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 552

QY 61 AACAGAAAGGTTTTGAGTACGGCTATAGCTGGACTTTCTGTGTGTACACCAATGCC 120
Db |||||
551 AACAGAAAGGTTTTGAGTACGGCTATAGCTGGACTTTCTGTGTGTACACCAATGCC 492

QY 121 CAACCTGCTGCTTAGGGTAGTGTAGGATCTCTGTCCATCAGCCAGGACAGTCAG 180
Db |||||
491 CAACCTGCTGCTTAGGGTAGTGTAGGATCTCTGTCCATCAGCCAGGACAGTCAG 432

QY 181 CTCTCTCTTTTTCAGGGCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 240
Db |||||
431 CTCTCTCTTTTTCAGGGCAATCCCGAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTC 372

QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC 300
Db |||||
371 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC 312

QY 301 TGTCACTGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db |||||
311 TGTCACTGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 252

QY 361 GTTTGTTTGTGATTCATTGTTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTA 420
Db |||||
251 GTTTGTTT-ATTCATTGTTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTA 193

QY 421 AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTCATTTGGAGCTGGTGTCTCTTT 480
Db |||||
192 AAAGAGCCTAGTTTTTAAATAGCTATGGAATCAATTCATTTGGAGCTGGTGTCTCTTT 133

QY 481 AAATCAAGTCCTTTAAATTAACACTGAAATATATATAAGCTCAGATTATTAAATGGGAATA 540
Db |||||
132 AAATCAAGTCCTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATA 73

QY 541 TTTATAATGAGCAAAATATGATCTGTTCAATGGTCTGAAATAAATCACTCACTGAAGAAA 600
Db |||||
72 TTTATAATGAGCAAAATATGATCTGTTCAATGGTCTGAAATAAATCACTCACTGAAGAAA 13

QY 601 AAAAAAAAAA 609
Db |||||
12 AAAAAAAAAA 4

RESULT 10
CA305984/c
LOCUS
DEFINITION
UI-H-FT1-bhs-f-05-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bhs-f-05-0-UI 3', mRNA sequence.
ACCESSION
CA305984
VERSION
CA305984.1 GI:24469035
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
REFERENCE
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhs-f-05-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 59.3%; Score 593.8; DB 14; Length 767;
Best Local Similarity 99.5%; Pred. No. 6.4e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
Db |||||
611 GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 552

QY	61	AAACAGAAAGCTTTTGGAGTACGGCTATAGCCTGGACCTTCTCTGTGTCTACACCAATGCC	120
Db	551	AAACAGAAAGCTTTTGGAGTACGGCTATAGCCTGGACCTTCTCTGTGTCTACACCAATGCC	492
QY	121	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	180
Db	491	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	432
QY	181	CTCTCTCCTTTTCAGGGCCAAATCCCGACGCTTTTGGAGCCAGGCTCTCTCACCTCTC	240
Db	431	CTCTCTCCTTTTCAGGGCCAAATCCCGACGCTTTTGGAGCCAGGCTCTCTCACCTCTC	372
QY	241	CTACTCACTTAAAGCCCGCTGACAGAAACCAAGGCTTGGTCTTAAGAAACCCCTC	300
Db	371	CTACTCACTTAAAGCCCGCTGACAGAAACCAAGGCTTGGTCTTAAGAAACCCCTC	312
QY	301	TGTCATTCGCTCCACATTCCTGATGAGCAACCGCTTCCCTATTTATTATTATTGTTT	360
Db	311	TGTCATTCGCTCCACATTCCTGATGAGCAACCGCTTCCCTATTTATTATTATTGTTT	252
QY	361	GTTTGTGTTTGAATTCATGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTCTGTA	420
Db	251	GTTTGTGTTT-ATTCAATGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTCTGTA	193
QY	421	AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT	480
Db	192	AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT	133
QY	481	AAATCAAGTCTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGAATA	540
Db	132	AAATCAAGTCTTTTAAATTAACACTGAAATATATAAGCTCAGATTATTTAAATGGAATA	73
QY	541	TTTATAAATGAGCAAAATATGACTGTTTCAATGGTTCTGAAATAACTTCACTGAAGAAA	600
Db	72	TTTATAAATGAGCAAAATATGACTGTTTCAATGGTTCTGAAATAACTTCACTGAAGAAA	13
QY	601	AAAAAAAAA 609	
Db	12	AAAAAAAAA 4	
RESULT 11			
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LOCUS			
DEFINITION			
UI-H-DP0-avr-h-12-0-UI.s1 NCI CGAP_Fs1 Homo sapiens cDNA clone			
UI-H-DP0-avr-h-12-0-UI 3', mRNA sequence.			
ACCESSION			
CA442834			
VERSION			
CA442834.1 GI:24807254			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 767)			
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
AUTHORS			
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
Tumor Gene Index			
JOURNAL			
Unpublished (1997)			
COMMENT			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs-r@mail.nih.gov			
Tissue Procurement: Dr. Mary Hendrix			
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa			
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa			
Clone Distribution: Clone distribution information can be obtained			
from Dr. M. Bento Soares, bento-soares@uiowa.edu			
The following repetitive elements were found in this cDNA			
sequence: 221-272, >(TAAA)n#Simple_repeat			
Seq primer: M13 FORWARD			
POLYA=Yes.			
FEATURES			
Location/Qualifiers			
1..767			
/organism="Homo sapiens"			
source			

/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="UI-H-DP0-avr-h-12-0-UI"			
/tissue_type="Fibrosarcoma"			
/lab_host="DH10B (Life Technologies)"			
/clone_lib="NCI CGAP_Fs1"			
/note="Vector: pT7T3-Pac (Pharmacia) with a modified			
polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_Fs1 is			
a cDNA library containing the following tissue(s):			
Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The			
library was constructed according to Bonaldo, Lennon and			
Soares, Genome Research, 6:791-806, 1996. First strand			
cDNA synthesis was primed with an oligo-dT primer			
containing a Not I site. Double stranded cDNA was ligated			
to an EcoR I adaptor, digested with Not I, and cloned			
directionally into pT7T3-Pac vector. The oligonucleotide			
used to prime the synthesis of first-strand cDNA contains			
a library tag sequence that is located between the Not I			
site and the (dT)18 tail. The sequence tag for this			
library is GTTCTACGAG.			
TAG_TISSUE=fibrosarcoma			
TAG_LIB=UI-H-DP0			
TAG_SEQ=GTTCTACGAG"			
ORIGIN			
Query Match 59.3%; Score 593.8; DB 14; Length 767;			
Best Local Similarity 99.5%; Pred. No. 6.4e-108;			
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;			
QY	1	GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	60
Db	611	GCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG	552
QY	61	AACAGAAAGGTTTGTAGTACGGCTATAGCCTGGACTTTCCTGTGTCTACACCAATGCC	120
Db	551	AACAGAAAGGTTTGTAGTACGGCTATAGCCTGGACTTTCCTGTGTCTACACCAATGCC	492
QY	121	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	180
Db	491	CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG	432
QY	181	CTCTCTCCTTTTCAGGGCCAAATCCCGACGCTTTTGTGGAGCCAGGCTCTCTCACCTCTC	240
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QY	241	CTACTCACTTAAAGCCCGCTGACAGAAACCAAGGCTTGGTCTTAAGAAACCCCTC	300
Db	371	CTACTCACTTAAAGCCCGCTGACAGAAACCAAGGCTTGGTCTTAAGAAACCCCTC	312
QY	301	TGTCATTCGCTCCACATTCCTGATGAGCAACCGCTTCCCTATTTATTATTATTGTTT	360
Db	311	TGTCATTCGCTCCACATTCCTGATGAGCAACCGCTTCCCTATTTATTATTATTGTTT	252
QY	361	GTTTGTGTTTGAATTCATGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTCTGTA	420
Db	251	GTTTGTGTTT-ATTCAATGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTCTGTA	193
QY	421	AAAGAGCCTAGTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTT	480
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Db	132	AAATCAAGTCTTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGAATA	73
QY	541	TTTATAAATGAGCAAAATATGACTGTTTCAATGGTTCTGAAATAACTTCACTGAAGAAA	600
Db	72	TTTATAAATGAGCAAAATATGACTGTTTCAATGGTTCTGAAATAACTTCACTGAAGAAA	13
QY	601	AAAAAAAAA 609	
Db	12	AAAAAAAAA 4	

RESULT 12
BQ000281/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BQ000281
UI-H-DP0-avt-c-13-0-UI.s1 NCI_CGAP_Fs1 Homo sapiens cDNA clone
IMAGE:5883972 3', mRNA sequence.
BQ000281
BQ000281.1 GI:19725181
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 770)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..770
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5883972"
/tissue_type="Fibrosarcoma"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Fs1"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_Fs1 is
a cDNA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTTCTACGAG.
TAG_TISSUE=fibrosarcoma
TAG_LIB=UI-H-DP0
TAG_SEQ=GTTCTACGAG"

ORIGIN
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Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1 GGTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60
611 GGTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 552
61 AACAGAAAGGTTTTTGAGTACGGCTATAGCTGGACTTTCCCTGTGTCTACACCAATGCC 120
551 AACAGAAAGGTTTTTGAGTACGGCTATAGCTGGACTTTCCCTGTGTCTACACCAATGCC 492
121 CAACTGCCTGCCTTAGGGTAGTGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
491 CAACTGCCTGCCTTAGGGTAGTGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 432

QY 181 CTCTCTCCTTTTCCAGGGCCCAATCCCGACCCCTTTTGTGTGAGCCAGGCCTCTCTCACCTCTC 240
Db 431 CTCTCTCCTTTTCCAGGGCCCAATCCCGACCCCTTTTGTGTGAGCCAGGCCTCTCTCACCTCTC 372
QY 241 CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTGGTTCTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTGGTTCTAAGAAACCCCTC 312
QY 301 TGTCACTTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTTATTATTATTGTTT 360
Db 311 TGTCACTTCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTTATTATTATTGTTT 252
QY 361 GTTTGTTTTCATTGCTGCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 420
Db 251 GTTTGTTTTCATTGCTGCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTA 193
QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGGCTCTCTTT 480
Db 192 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGGCTCTCTTT 133
QY 481 AAATCAAGTCCTTTAATTAACACTCAAAAATATATAAGCTCAGATTATTTAAATGGGAATA 540
Db 132 AAATCAAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATA 73
QY 541 TTTATAATGAGCAAAATATGATGACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAA 600
Db 72 TTTATAATGAGCAAAATATGATGACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAA 13
QY 601 AAAAAA 609
Db 12 AAAAAA 4

RESULT 13
CA431534/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
CA431534
UI-H-FT0-bhm-o-03-0-UI.s1 NCI_CGAP_FTO Homo sapiens linear EST 07-NOV-2002
UI-H-FT0-bhm-o-03-0-UI 3', mRNA sequence.
CA431534
CA431534.1 GI:24794254
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 777)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..777
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT0-bhm-o-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FTO"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT0 is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa.

TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 59.3%; Score 593.8; DB 14; Length 777;
Best Local Similarity 99.5%; Pred. No. 6.3e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	1	GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	60
Db	611	GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	552
QY	61	AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGAGCTTTCCTGTGTCTACACCAATGCC	120
Db	551	AACAGAAAGGTTTTTGTAGTACGGCTATAGCCCTGAGCTTTCCTGTGTCTACACCAATGCC	492
QY	121	CAACTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCTCTGTCCATCAGCAGGACAGTCAG	180
Db	491	CAACTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCTCTGTCCATCAGCAGGACAGTCAG	432
QY	181	CTCTCTCCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	240
Db	431	CTCTCTCCTTTCAGGGCCCAATCCCGAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC	372
QY	241	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCACATTTGGTTCTAAGAAACCCCTC	300
Db	371	CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCACATTTGGTTCTAAGAAACCCCTC	312
QY	301	TGTCATTCGCTCCACATTCGTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT	360
Db	311	TGTCATTCGCTCCACATTCGTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT	252
QY	361	GTTTGTGTTTCAATTCATTGGTCTAAATTTATTCAAAGGGGCAAGAGTAGAGTGTCTGTA	420
Db	251	GTTTGTGTTT-ATTCAATTGGTCTAAATTTATTCAAAGGGGCAAGAGTAGAGTGTCTGTA	193
QY	421	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT	480
Db	192	AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTT	133
QY	481	AAATCAAGTCTCTTTAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	540
Db	132	AAATCAAGTCTCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA	73
QY	541	TTTATAAATGAGCAAAATATGATCTGTTCAATGGTTCGAAATAAACTTCACTGAAGAAA	600
Db	72	TTTATAAATGAGCAAAATATCATACTGTTCATGTTTCAATGGTTCGAAATAAACTTCACTGAAGAAA	13
QY	601	AAAAAAAAA	609
Db	12	AAAAAAAAA	4

RESULT 14
CA307234/c
LOCUS

CA307234 798 bp mRNA linear EST 01-NOV-2002

DEFINITION UI-H-FT1-bhu-p-02-0-UI.s1 NCI CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bhu-p-02-0-UI 3', mRNA sequence.
CA307234
VERSION CA307234.1 GI:24470288
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 798)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers

1..798
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-p-02-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 59.3%; Score 593.8; DB 14; Length 798;
Best Local Similarity 99.5%; Pred. No. 6.3e-108;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	1	GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	60
Db	611	GCTGTACCCAGAGAGTCTCTGTGCTGAATGTGGACTCAATCCCTAGGCTGGCAGAAAGG	552
QY	61	AACAGAAAGGTTTTTGTAGTACGGCTATAGCTTTCCTGTGTCTACACCAATGCC	120
Db	551	AACAGAAAGGTTTTTGTAGTACGGCTATAGCTTTCCTGTGTCTACACCAATGCC	492
QY	121	CAACTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCAG	180
Db	491	CAACTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCTGTCCATCAGCAGGACAGTCAG	432

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QY 181 CTCTCTCCTTTCCAGGGCCAAATCCCCAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC 240
Db 431 CTCTCTCCTTTCCAGGGCCAAATCCCCAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC 372
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGCCACATTTGGTCTTAAGAAACCCCTC 312
QY 301 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db 311 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 252
QY 361 GTTTGTTTGAATTCATTTGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGAGTGTCTGTA 420
Db 251 GTTTGTTT-ATTCAATGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGAGTGTCTGTA 193
QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAAATTTGGACTGGTGTCTCTCTT 480
Db 192 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAAATTTGGACTGGTGTCTCTCTT 133
QY 481 AAATCAAGTCCTTTAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 540
Db 132 AAATCAAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 73
QY 541 TTTATAATGAGCAAAATATGATGACTGTTCAATGGTCTGAAATATAAATCACTGAAGAAA 600
Db 72 TTTATAATGAGCAAAATATGATGACTGTTCAATGGTCTGAAATATAAATCACTGAAGAAA 13
QY 601 AAAAAAAAAA 609
Db 12 AAAAAAAAAA 4
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RESULT 15

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BQ001221/c
LOCUS BQ001221 703 bp mRNA linear EST 17-JUN-2002
DEFINITION UI-H-DH1-awp-g-21-0-UI.s1 NCI_CGAP_DH1 Homo sapiens CDNA clone
IMAGE:5892524 3', mRNA sequence.
ACCESSION BQ001221
VERSION BQ001221.1 GI:19726121
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 703)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 221-272. >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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FEATURES

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source
1..703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5892524"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_DH1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
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modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC.

TAG_TISSUE=lung
TAG_LIB=UI-H-DH1
TAG_SEQ=AGATCATTGC"

ORIGIN

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Query Match 59.2%; Score 592.8; DB 12; Length 703;
Best Local Similarity 99.3%; Pred. No. 1.le-107;
Matches 605; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GCTGTACCCAGAGAGTCCCTGCTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 60
Db 611 GCTGTACCCAGAGAGTCCCTGCTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGG 552
QY 61 AACAGAAAGGTTTTTGGAGTAGCGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 120
Db 551 AACAGAAAGGTTTTTGGAGTAGCGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCC 492
QY 121 CAACTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 180
Db 491 CAACTGCCTGCCTTAGGGTAGTCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG 432
QY 181 CTCTCTCCTTTTCAGGGCCAAATCCCCAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC 240
Db 431 CTCTCTCCTTTTCAGGGCCAAATCCCCAGCCCTTTTGTGTGAGCCAGGCTCTCTCACCTCTC 372
QY 241 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCCACATTTGGTCTTAAGAAACCCCTC 300
Db 371 CTACTCACTTAAAGCCCGCTGACAGAAACCCAGGCCACATTTGGTCTTAAGAAACCCCTC 312
QY 301 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 360
Db 311 TGTCAATCGCTCCACATTTCTGATGAGCAACCGCTTCCCTATTATTATTATTATTGTTT 252
QY 361 GTTTGTTTGAATTCATTTGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGAGTGTCTGTA 420
Db 251 GTTTGTTT-ATTCAATGGTCTAAATTTATTCAAAGGGGGCAAGAGTAGAGTGTCTGTA 193
QY 421 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAAATTTGGACTGGTGTCTCTCTT 480
Db 192 AAAGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAAATTTGGACTGGTGTCTCTCTT 133
QY 481 AAATCAAGTCCTTTAATTAACACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 540
Db 132 AAATCAAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATA 73
QY 541 TTTATAAATGAGCAAAATATGATGACTGTTCAATGGTCTGAAATATAAATCACTGAAGAAA 600
Db 72 TTTATAAATGAGCAAAATATGATGACTGTTCAATGGTCTGAAATATAAATCACTGAAGAAA 13
QY 601 AAAAAAAAAA 609
Db 12 AAAAAAAAAA 4
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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 20:32:30 ; Search time 1145 Seconds
(without alignments)
5998.482 Million cell updates/sec

Title: US-09-247-874C-2_COPY_8710_8945
Perfect score: 236
Sequence: 1 ttttgattcattgttctaatt.....ataaacttcaactgaagaaaa 236

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 7: gb_ph.*
- 8: gb_pl.*
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- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 23: em_pat.*
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- 32: em_htg_other.*
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- 34: em_htg_pln.*
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- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	194	82.2	614	11	G10509	G10509 human STS C
2	194	82.2	656	6	AX027920	AX027920 Sequence
3	194	82.2	1469	6	I01156	I01156 Sequence 1
4	194	82.2	1496	9	HUMIL1	K02770 Human monoc
5	194	82.2	1496	9	HUMIL1C	M54933 Human monoc
6	194	82.2	1507	6	E00846	E00846 cDNA sequen
7	194	82.2	1507	6	I07942	I07942 Sequence 1
8	194	82.2	9721	6	AX052806	AX052806 Sequence
9	194	82.2	9721	6	AX067266	AX067266 Sequence
10	194	82.2	9721	6	AX469435	AX469435 Sequence
11	194	82.2	9721	9	HSIL1B	X04500 Human gene
12	189	80.1	1382	6	AX419978	AX419978 Sequence
13	189	80.1	1473	9	HSPRO11B	X56087 Human mRNA
14	189	80.1	1497	6	AR030386	AR030386 Sequence
15	189	80.1	1497	6	E06734	E06734 DNA encodin
16	189	80.1	1497	9	HUMIL1BA	M15330 Human inter
17	189	80.1	1522	9	BC008678	BC008678 Homo sapi
18	189	80.1	7824	9	HUMIL1B	M15840 Human inter
19	189	80.1	17447	9	AY137079	AY137079 Homo sapi
20	189	80.1	154214	9	AC079753	AC079753 Homo sapi
21	132	55.9	1514	6	AR086959	AR086959 Sequence
22	132	55.9	1514	6	I00729	I00729 Sequence 2
23	121	51.3	1404	6	A21148	A21148 pGIF- alpha
24	121	51.3	1404	6	E01230	E01230 cDNA encodi
25	121	51.3	1404	6	E11934	E11934 cDNA encodi
26	121	51.3	1404	6	E12090	E12090 Human cDNA
27	121	51.3	1404	6	I00228	I00228 Sequence 2
28	41	17.4	1458	6	E02498	E02498 cDNA encodi
29	30	12.7	400	11	G13631	G13631 SHGC-11912
30	22	9.3	1377	4	RAB11B	M26295 Rabbit inte
31	22	9.3	1403	4	RAB11B2	D21835 Rabbit mRNA
32	22	9.3	23104	2	AC017874	AC017874 Drosophil
33	22	9.3	171226	3	AC008144	AC008144 Drosophil
34	22	9.3	238245	3	AE003737	AE003737 Drosophil
35	21	8.9	150956	2	AC117259	AC117259 Mus muscu
36	21	8.9	155020	2	AC106390	AC106390 Rattus no
37	20	8.5	56870	9	AL512822	AL512822 Human DNA
38	20	8.5	59728	2	AC104292	AC104292 Rattus no
39	20	8.5	70849	2	AC090139	AC090139 Homo sapi
40	20	8.5	91242	9	AP001252	AP001252 Homo sapi
41	20	8.5	105495	9	AC105999	AC105999 Homo sapi
42	20	8.5	105496	9	AF165142	AF165142 Homo sapi
43	20	8.5	120038	9	AC020551	AC020551 Homo sapi
44	20	8.5	126117	2	AL157949	AL157949 Homo sapi
45	20	8.5	140409	2	AC044825	AC044825 Homo sapi

ALIGNMENTS

RESULT 1	G10509	human STS CHLC.UTR_00699_X04500.0.P37183 clone UTR_00699_X04500,	614 bp	DNA	linear	STS 15-AUG-1995
LOCUS	G10509	sequence tagged site.				
DEFINITION	G10509	human STS CHLC.UTR_00699_X04500.0.P37183 clone UTR_00699_X04500,				
ACCESSION	G10509	GI:942358				
VERSION	G10509.1	GI:942358				
KEYWORDS	STS; STS sequence; primer; sequence tagged site.					
SOURCE	Homo sapiens vector=pJCP1 host=E.coli dut+ung+ (DH10B) Marker					
ORGANISM	Selected genomic DNA prepared from XY individual of French nationality.					
REFERENCE	1 (bases 1 to 614)					

AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: UTR_00699_X04500, CHLC.UTR_00699_X04500.T36097
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu

Primer A: AGTCAGCTCTCTCCTTCAGG
Primer B: CTTGCCCTCTTTGAATAAT
STS size: 229
PCR Profile:

denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C

Protocol:

Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 ul

Buffer:

MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3

Prepared with primer pairs derived from X04500.

Location/Qualifiers

1. .614
/organism="Homo sapiens"
/db_xref="taxon:9606"

STS primer_bind 180. .408
primer_bind 180. .200
complement(389..408) 184 t
BASE COUNT 174 a 136 c 120 g 184 t
ORIGIN

Query Match 82.2%; Score 194; DB 11; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.9e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTTCATTTGCTCTAATTTATTCAGGGGGCAAGAGTAGCAGTGCTCTGTAAGA 60
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QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGCTCTCTTTAAATC 120
Db 431 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGCTCTCTTTAAATC 490
QY 121 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
Db 491 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 550

QY 181 AAATGAGCAAAATAT 194
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RESULT 2 AX027920 AX027920 656 bp DNA linear PAT 16-SEP-2000
LOCUS AX027920 Sequence 5 from Patent WO0039314.
DEFINITION AX027920
ACCESSION AX027920
VERSION AX027920.1 GI:10188746
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 656)
AUTHORS Kastelic, T. and Cheneval, D.
TITLE Assay for identifying compounds which affect stability of mrna
JOURNAL Patent: WO 0039314-A 5 06-JUL-2000;
KASTELIC TANIA (CA); CHENEVAL DOMINIQUE (CA); NOVATION
PHARMACEUTICALS INC (CA)
FEATURES Location/Qualifiers
1. .656
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/db_xref="taxon:9606"
BASE COUNT 176 a 151 c 129 g 200 t
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Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTTCATTTGCTCTAATTTATTCAGGGGGCAAGAGTAGCAGTGCTCTGTAAGA 60
Db 429 TTTTGATTTCATTTGCTCTAATTTATTCAGGGGGCAAGAGTAGCAGTGCTCTGTAAGA 488
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGCTCTCTTTAAATC 120
Db 489 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGCTCTCTTTAAATC 548
QY 121 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
Db 549 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 608
QY 181 AAATGAGCAAAATAT 194
Db 609 AAATGAGCAAAATAT 622

RESULT 3 I01156 I01156 1469 bp ss-DNA linear PAT 21-MAY-1993
LOCUS I01156 Sequence 1 from Patent US 4762914.
DEFINITION I01156
ACCESSION I01156
VERSION I01156.1 GI:313921
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1469)
AUTHORS Auron, P.E., Webb, A.C., Gehrke, L., Dinarello, C.A., Rosenwasser, L.J., Rich, A. and Wolff, S.M.
TITLE Truncated protein of interleukin-1
JOURNAL Patent: US 4762914-A 1 09-AUG-1988;
119 Wilson Dr.; Framingham, MA
COMMENT On Jul 30, 1993 this sequence version replaced gi:285486.
FEATURES Location/Qualifiers
1. .1469
source /organism="unknown"
BASE COUNT 408 a 354 c 326 g 381 t
ORIGIN

Query Match 82.2%; Score 194; DB 6; Length 1469;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGCTCTCTTTAAATC 120
Db 1328 GCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGCTCTCTTTAAATC 1387

QY 121 AAGTCCTTTAATTAGACTGAAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 180
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QY 181 AAATGAGCAAAATAT 194
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Db 1448 AAATGAGCAAAATAT 1461
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RESULT 4
HUMIL1
LOCUS Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
DEFINITION K02770
ACCESSION K02770
VERSION K02770.1 GI:186268
KEYWORDS interleukin; interleukin 1.
SOURCE Human endotoxin-stimulated monocyte, cDNA to mRNA, clones pA-26, pcD-415 and pcD-1218.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1496)
AUTHORS Auron,P.E., Webb,A.C., Rosenwasser,L.J., Mucci,S.F., Rich,A., Wolff,S.M. and Dinarello,C.A.
TITLE Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7907-7911 (1984)
MEDLINE 85088517
PUBMED 6083565
COMMENT A potential poly-A signal is found at position 1484-1489. Two basic sequences that could be sites for protein processing, similar to those observed for peptide hormones, are found at positions 708-716 and 723-728.
FEATURES
source
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/db_xref="taxon:9606"
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87..896
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/db_xref="GI:307043"
/translation="MAEVPKLASEMMAYSGNEDDLFFFEADGPKQMKCSFQDLDLCP
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SFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKMEKRFVFN
KIEINKLEFESAOFPNWIYSTQAEENMPVFLGGTKGGQDITDFTMQFVSS"
BASE COUNT 416 a 361 c 328 g 391 t
ORIGIN 104 bp upstream of AluI site.
Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATGGTCTAATTTATTCAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 60
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Db 1269 TTTTGATTCAATGGTCTAATTTATTCAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 1328
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QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 120
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QY 121 AAGTCCTTTAATTAAGACTGAAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 180
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QY 181 AAATGAGCAAAATAT 194
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Db 1449 AAATGAGCAAAATAT 1462
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RESULT 5
HUMIL1
LOCUS Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
DEFINITION K02770
ACCESSION K02770
VERSION K02770.1 GI:186268
KEYWORDS interleukin; interleukin 1.
SOURCE Human endotoxin-stimulated monocyte, cDNA to mRNA, clones pA-26, pcD-415 and pcD-1218.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1496)
AUTHORS Auron,P.E., Webb,A.C., Rosenwasser,L.J., Mucci,S.F., Rich,A., Wolff,S.M. and Dinarello,C.A.
TITLE Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7907-7911 (1984)
MEDLINE 85088517
PUBMED 6083565
COMMENT A potential poly-A signal is found at position 1484-1489. Two basic sequences that could be sites for protein processing, similar to those observed for peptide hormones, are found at positions 708-716 and 723-728.
FEATURES
source
1..1496
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87..896
/note="interleukin 1 precursor polypeptide"
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KIEINKLEFESAOFPNWIYSTQAEENMPVFLGGTKGGQDITDFTMQFVSS"
BASE COUNT 416 a 361 c 328 g 391 t
ORIGIN 104 bp upstream of AluI site.
Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATGGTCTAATTTATTCAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 60
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Db 1269 TTTTGATTCAATGGTCTAATTTATTCAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 1328
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QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 120
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Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 1388
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QY 121 AAGTCCTTTAATTAAGACTGAAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 180
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Db 1389 AAGTCCTTTAATTAAGACTGAAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 1448
|||||
QY 181 AAATGAGCAAAATAT 194
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Db 1449 AAATGAGCAAAATAT 1462
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RESULT 5

HUMIL1C
LOCUS Human monocyte interleukin mRNA, complete cds.
DEFINITION M54933 M38756
ACCESSION M54933.1 GI:186287
KEYWORDS interleukin 1.
SOURCE Human monocyte, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1496)
AUTHORS Webb,A.C., Dinarello,C.A., Rosenwasser,L.J., Mucci,S.F., Rich,A., Wolff,S.M. and Auron,P.E.
TITLE Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
JOURNAL Adv. Gene Technol. 22, 339-340 (1985)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
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88..897
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BASE COUNT 416 a 367 c 322 g 391 t
ORIGIN
Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATGGTCTAATTTATTCAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 60
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|||||
QY 121 AAGTCCTTTAATTAAGACTGAAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 180
|||||
Db 1389 AAGTCCTTTAATTAAGACTGAAAAATATATAAGCTCAGATTATTAAATGGGAATATTTAT 1448
|||||
QY 181 AAATGAGCAAAATAT 194
|||||
Db 1449 AAATGAGCAAAATAT 1462
|||||
RESULT 6
E00846
LOCUS CDNA sequence for human IL-1.
DEFINITION E00846
ACCESSION E00846
VERSION E00846.1 GI:2169107
KEYWORDS JP 1986119191-A/1.
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1507)
AUTHORS Fuiritsupu,I.A., Chiyaarusu,E.D., Andoriyuu,S.U., Arekisandaa,R., Shierudon,E.U., Rii,G. and Rani,J.R.
TITLE HUMAN IL-1CDNA HAVING BIOLOGICALLY ACTIVE HUMAN IL-1 PROTEINCODE
JOURNAL Patent: JP 1986119191-A 1 06-JUN-1986;
MASSACHUSETTS INST OF TECHNOLOG <MIT>, NEW INGUARDO MEDICAL CENTER
HOSUPITARUZU INC, TRUSTEES OBU TAFUTSU KARETSUJI, UERESUREI
KARETSUJI
COMMENT OS Human (Homo sapiens)
PN JP 1986119191-A/1
PD 06-JUN-1986
PF 18-MAY-1985 JP 1985104978
PR 18-MAY-1984 US 84 611669, 11-FEB-1985 US 85 700374 PI
FUIRITSUPU II AURON, CHIYAARUSU EE DEINARERO, PI ANDORIYUU SHII
UEBU,
PI AREKISANDAA RITSUCHI, SHIERUDON EMU UORUFU, RII GEERUKE, PI
RANII JIEE ROOZENWATSUSAA
PC C12N15/00,A61K39/395,C07K13/00,C12N1/00,C12N5/00,C12P21/02, PC
(C12N1/00,
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=Blood;
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FH key Location/Qualifiers
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FT CDS 87..896
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FT polyA signal 1484..1489.
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Db 1269 TTTTGATTTCATGGTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 1328
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGAGTGGTGTCTCTTTAAATC 120
Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGAGTGGTGTCTCTTTAAATC 1388
QY 121 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTTTAAATGGGAATATTAT 180
Db 1389 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTTTAAATGGGAATATTAT 1448
QY 181 AAATGAGCAAATAT 194
Db 1449 AAATGAGCAAATAT 1462
RESULT 8
AX052806 9721 bp DNA linear PAT 12-JAN-2001
LOCUS AX052806
DEFINITION Sequence 16 from Patent WO0071753.
ACCESSION AX052806
VERSION AX052806.1 GI:12226963
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9721)
AUTHORS Kornman,K.S., Duff,G.W., Crossman,D.C., Francis,S.E. and Stephenson,K.
TITLE Diagnostics and therapeutics for restenosis
JOURNAL Patent: WO 0071753-A 16 30-NOV-2000;
Interleukin Genetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..9721
/organism="Homo sapiens"
/db xref="taxon:9606"
/note="IL-1B gene-'n' bases throughout the sequence may be A, T, C, G, other or Unknown"
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Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTTCATGGTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60
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QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGAGTGGTGTCTCTTTAAATC 120

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1507)
AUTHORS Auron,P.E., Webb,A.C., Gehrke,L., Dinarello,C.A., Rosenwasser,L.J., Rich,A. and Wolff,S.M.
TITLE Human il-1 cDNA sequences encoding biologically-active human il-1 proteins
JOURNAL Patent: EP 0161901-A2 1 21-NOV-1985;
FEATURES Location/Qualifiers
source 1..1507
/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1269 TTTTGATTTCATGGTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 1328
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGAGTGGTGTCTCTTTAAATC 120
Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGAGTGGTGTCTCTTTAAATC 1388
QY 121 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTTTAAATGGGAATATTAT 180
Db 1389 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTTTAAATGGGAATATTAT 1448
QY 181 AAATGAGCAAATAT 194
Db 1449 AAATGAGCAAATAT 1462
RESULT 8
AX052806 9721 bp DNA linear PAT 12-JAN-2001
LOCUS AX052806
DEFINITION Sequence 16 from Patent WO0071753.
ACCESSION AX052806
VERSION AX052806.1 GI:12226963
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9721)
AUTHORS Kornman,K.S., Duff,G.W., Crossman,D.C., Francis,S.E. and Stephenson,K.
TITLE Diagnostics and therapeutics for restenosis
JOURNAL Patent: WO 0071753-A 16 30-NOV-2000;
Interleukin Genetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..9721
/organism="Homo sapiens"
/db xref="taxon:9606"
/note="IL-1B gene-'n' bases throughout the sequence may be A, T, C, G, other or Unknown"
BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN
Query Match 82.2%; Score 194; DB 6; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 8710 TTTTGATTTCATGGTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 8769
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Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 8710 TTTTGATTGCTGCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGA 8769
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Db 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTTTAAATC 8829
QY 121 AAGTCCTTTAATTAAGACTGAAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
Db 8830 AAGTCCTTTAATTAAGACTGAAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 8889
QY 181 AAATGAGCAAAATAT 194
Db 8890 AAATGAGCAAAATAT 8903

RESULT 12
AX419978      AX419978      1382 bp      mRNA      linear      PAT 18-JUN-2002
LOCUS
DEFINITION   Sequence 315 from Patent WO0198537.
ACCESSION   AX419978
VERSION      AX419978.1  GI:21524345
KEYWORDS     human.
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Lyamichev, V., Allawi, H., Dong, F., Neri, B.P. and Vener, I.T.
TITLE        Nucleic acid accessible hybridization sites
JOURNAL      Patent: WO 0198537-A 315 27-DEC-2001;
              THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES     Location/Qualifiers
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              /db_xref="taxon:9606"
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ORIGIN
Query Match      80.1%; Score 189; DB 6; Length 1382;
Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1183 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 1242
QY 66 GTTTTAAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
Db 1243 GTTTTAAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATCAAGTC 1302
QY 126 CTTTAATTAAGACTGAAAATATATATAAGCTCAGATTATTTAAATGGGAATATTATAAATG 185
Db 1303 CTTTAATTAAGACTGAAAATATATATAAGCTCAGATTATTTAAATGGGAATATTATAAATG 1362
QY 186 AGCAAAATAT 194
Db 1363 AGCAAAATAT 1371

RESULT 13
HSPRO11B      HSPRO11B      1473 bp      mRNA      linear      PRI 06-DEC-1990
LOCUS
DEFINITION   Human mRNA for prointerleukin 1 beta.
ACCESSION   X56087
VERSION      X56087.1  GI:35662
KEYWORDS     prointerleukin 1; prointerleukin 1 beta.
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 1473)
AUTHORS      Kotenko, S.V., Bulenikov, M.T., Veiko, V.P., Epishin, S.M.,
```

Lomakin,I.B., Emel'yanov,A.V., Kozlov,A.P., Konusova,V.G.,
Kotov,A.Y., Kurbatova,T.V., Reshetnikov,V.L., Simbirtsev,A.S.,
Ketlinskii,S.A. and Vinetskii,Y.P.
Cloning of the cDNA coding for human prointerleukin-1 alpha and
prointerleukin-1 beta
Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989)
90249285
PUBMED 2635664

FEATURES
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Location/Qualifiers
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/gene="proIL-1 beta"
58..867
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Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 65
Db 1242 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 1301
QY 66 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTTTAAATCAAGTC 125
Db 1302 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTTTAAATCAAGTC 1361
QY 126 CTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTATAAATG 185
Db 1362 CTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTATAAATG 1421
QY 186 AGCAAAATAT 194
Db 1422 AGCAAAATAT 1430

RESULT 14
AR030386
LOCUS AR030386 1497 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5861267.
ACCESSION AR030386
VERSION AR030386.1 GI:5943600
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1497)
AUTHORS Su,M.
TITLE Methods, nucleotide sequences and host cells for assaying exogenous
and endogenous protease activity
JOURNAL Patent: US 5861267-A 10 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..1497

BASE COUNT 411 a 365 c 331 g 390 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 65
Db 1271 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 1330
QY 66 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTTTAAATCAAGTC 125
Db 1331 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTTTAAATCAAGTC 1390
QY 126 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
Db 1391 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 1450
QY 186 AGCAAAATAT 194
Db 1451 AGCAAAATAT 1459

RESULT 15
E06734
LOCUS E06734 DNA encoding IL-1 beta.
DEFINITION E06734
ACCESSION E06734
VERSION E06734.1 GI:2174916
KEYWORDS JP 1994041185-A/5.
SOURCE Unidentified.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1497)
AUTHORS Higaki,M., Shoji,Y. and Mizushima,Y.
TITLE OHOSPHOOLIGONUCLEOTIDE AND ITS USE
JOURNAL Patent: JP 1994041185-A 5 15-FEB-1994;
L T T KENKUSHO:KK
COMMENT PN JP 1994041185-A/5
PD 15-FEB-1994
PF 16-JUL-1992 JP 1992213519
PI HIGAKI MEGUMI, SHOJI YOKO, MIZUSHIMA YUTAKA
PC C07H21/04,A61K31/70,A61K31/70,C12P19/34;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT mat_peptide 1..1497
FT /product='IL-1 beta'.
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source 1..1497
/organism="synthetic construct"
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BASE COUNT 411 a 365 c 331 g 390 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 65
Db 1271 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 1330
QY 66 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTTTAAATCAAGTC 125
Db 1331 GTTTTAAATAGCTATGGAATCAATTCAATTGGACTGGTGTCTCTTTAAATCAAGTC 1390
QY 126 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
Db 1391 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 1450

QY 186 AGCAAAATAT 194
|||
Db 1451 AGCAAAATAT 1459

Search completed: March 17, 2003, 21:05:13
Job time : 1157 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 19:52:45 ; Search time 224 Seconds
(without alignments)
2372.641 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	236	100.0	9721	21	Human interleukin-1
2	194	82.2	656	21	Interleukin 1-beta
3	194	82.2	1496	21	Human interleukin-
4	194	82.2	1496	21	Human adenosine re
5	194	82.2	1507	6	Sequence encoding
6	194	82.2	1507	14	Human interleukin-
7	194	82.2	9721	20	Human interleukin
8	194	82.2	9721	21	Human interleukin-
9	194	82.2	9721	21	Human IL-1B gene.

10	194	82.2	9721	21	AAA50174	Human interleukin-
11	194	82.2	9721	21	AAA34823	Human adenosine re
12	194	82.2	9721	22	AAF27666	IL-1B DNA. Uniden
13	194	82.2	9721	22	AAC91434	Human IL-1B nucleo
14	194	82.2	9721	24	AAD35192	Human prointerleuk
15	194	82.2	29433	21	AAF20950	Human interleukin-
16	194	82.2	29433	21	AAA34828	Human adenosine re
17	194	82.2	209273	21	AAF21437	Human factor-relat
18	189	80.1	1382	24	ABL46348	Human interleukin-
19	189	80.1	1497	21	AAF20944	Human interleukin-
20	189	80.1	1497	21	AAA34822	Human adenosine re
21	189	80.1	1497	24	ABK83933	Human cDNA differe
22	189	80.1	7824	16	AAQ74052	Human interleukin-
23	189	80.1	7824	22	AAH24368	Human IL1B gene.
24	189	80.1	7824	24	ABK50291	Human interleukin
25	189	80.1	7824	24	ABK50293	Human interleukin
c 26	189	80.1	14690	20	AAAX22303	Human IL-1ra BAC c
27	138	58.5	1497	15	AAQ58462	IL-1 beta gene.
28	132	55.9	1514	21	AAZ55973	cDNA encoding huma
29	125	53.0	454	16	AAT20507	Human gene signatu
30	121	51.3	1404	7	AAN60283	Sequence encoding
31	121	51.3	1404	8	AAN70505	Sequence encoding
32	121	51.3	1404	14	AAQ51110	Human interleukin-
33	58	24.6	60	24	ABN38537	Human spliced tran
34	44	18.6	44	21	AAA50182	Probe used to dete
c 35	44	18.6	44	21	AAA50184	Probe used to dete
36	41	17.4	1458	11	AAQ05593	Monkey IL-2 beta g
c 37	33	14.0	8639	20	AAAX02995	Human IL-1ra BAC c
c 38	24	10.2	44	21	AAA50183	Probe used to dete
39	23	9.7	42	21	AAA50181	Probe used to dete
c 40	22	9.3	2983	23	ABL09950	Drosophila melanog
41	21	8.9	21	21	AAA50179	Primer used to det
c 42	20	8.5	28	21	AAA50180	Primer used to det
c 43	20	8.5	32	21	AAA50178	Primer used to det
44	19	8.1	579	24	ABQ35686	Oligonucleotide fo
c 45	19	8.1	579	24	ABQ35687	Oligonucleotide fo

ALIGNMENTS

RESULT 1
AAA50175
ID AAA50175 standard; DNA; 9721 BP.
XX
AC AAA50175;
XX 07-NOV-2000 (first entry)
XX Human interleukin-1 beta allele 2 (+6912).
KW Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;
KW coronary artery disease; osteoporosis; nephropathy;
KW alopecia areata; Graves disease; systemic lupus erythematosus;
KW lichen sclerosis; ulcerative colitis; diabetic retinopathy;
KW periodontal disease; juvenile chronic arthritis; psoriasis;
KW insulin dependent diabetes; asthma; lung fibrosis;
KW chronic inflammatory liver disease; rheumatoid arthritis;
KW chronic inflammatory lung disease; antiinflammatory; osteopathic;
KW dermatological; immunosuppressive; antidiabetic; antithyroid;
KW antiarthritic; antiarheumatic; antiasthmatic; antipsoriatic;
KW hepatotropic; antiulcer; diagnosis; therapy; ds.
XX Homo sapiens.

Key	Location/Qualifiers
variation	replace(8904,C)
FT	/*tag= a
FT	/note= "IL-1B allele 2 (+6912)"
XX	
PN	WO200047619-A1.
XX	
PD	17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03443.
XX 10-FEB-1999; 99US-0247874.
XX (INTE-) INTERLEUKIN GENETICS INC.
XX Duff GW, Di Giovine FS;
XX WPI; 2000-558192/51.
XX Novel methods and nucleic acids for diagnosing and treating disorders
PT associated with high levels of interleukin 1beta, especially
PT inflammatory diseases -
XX
XX Claim 34; Fig 2; 74pp; English.
XX
CC The present sequence is that of human interleukin-1 beta (IL-1B)
CC allele 2 (+6912), which is a form of the IL-1B gene that contains
CC guanine at position +6912; IL-1B allele 1 (+6912) has cytosine at
CC this position (see AAA50174). The invention is based on the
CC identification of this novel allele at marker +6912 of the IL-1B
CC gene. The C to G transition occurs within the 3' untranslated
CC region of the IL-1B gene and results in an increased level of IL-1B
CC protein. Individuals homozygous for the IL-1B allele 2 (+6912)
CC accumulate approximately 4 times more immunoreactive IL-1B protein
CC than homozygotes for IL-1B allele 1 (+6912). Methods and kits are
CC provided for detecting IL-1B allele 2 (+6912), or an allele in
CC linkage disequilibrium with an IL-1B allele 2 (+6912), and
CC thereby determining a patient's susceptibility to developing
CC inflammatory disorders, especially coronary artery disease,
CC osteoporosis, nephropathy in diabetes mellitus, alopecia areata,
CC Graves disease, systemic lupus erythematosus, lichen sclerosis,
CC ulcerative colitis, diabetic retinopathy, periodontal disease,
CC juvenile chronic arthritis, psoriasis, insulin dependent diabetes,
CC asthma, chronic inflammatory liver disease, chronic inflammatory
CC lung disease, lung fibrosis, and rheumatoid arthritis (claimed).
CC Identification of the IL-1B allele 2 (+6912) and its involvement in
CC IL-1B overproduction also enables screening assays for identifying
CC IL-1B antagonists that can be used to treat conditions associated
CC with IL-1B allele 2 (+6912). Transgenic animals are also claimed,
CC and can be used to identify IL-1B agonists and antagonists, or
CC to confirm the safety and efficacy of candidate therapeutics.
XX
SQ Sequence 9721 BP; 2661 A; 2327 C; 2123 G; 2608 T; 2 other;
Query Match 100.0%; Score 236; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATGGTCTAATTTATTCAGAGGGGGCAAGTAGCAGTGTCTCTAAAGA 60
Db TTTTGATTCAATGGTCTAATTTATTCAGAGGGGGCAAGTAGCAGTGTCTCTAAAGA 8769
QY 61 GCCTAGTTTAAATAGCTATGGAATCAATTTGAGTGGTGTCTCTCTTAAATC 120
Db GCCTAGTTTAAATAGCTATGGAATCAATTTGAGTGGTGTCTCTCTTAAATC 8829
QY 121 AAGTCCTTTAATAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGATATTAT 180
Db AAGTCCTTTAATAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGATATTAT 8889
QY 181 AAATGAGCAAAATGATACCTGTTCAATGGTCTCTGAAATAAAGTCACTGAAGAAA 236
Db AAATGAGCAAAATGATACCTGTTCAATGGTCTCTGAAATAAAGTCACTGAAGAAA 8945
RESULT 2
AAA51659
ID AAA51659 standard; cDNA; 656 BP.
XX
AC
XX AAA51659;

DT 31-OCT-2000 (first entry)
XX Interleukin 1-beta 3' UTR cDNA.
XX
KW IL-1-beta; 3' UTR; interleukin 1-beta; AU-rich element; ARE motif;
KW mRNA instability; rheumatoid arthritis; osteoarthritis; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT repeat_region 404..416
FT /*tag= a
FT /rpt_type= TANDEM
FT /note= "3 copies of AU-rich motif"
FT repeat_unit 404..408
FT /*tag= b
FT /note= "AU-rich motif"
FT misc_feature 406..414
FT /*tag= c
FT polyA_signal 644..649
FT /note= "Minimal instability motif"
FT /*tag= d
XX WO2000039314-A1.
PN 06-JUL-2000.
XX 23-DEC-1999; 99WO-CA01235.
XX 24-DEC-1998; 98GB-0028709.
XX (NOVA-) NOVATION PHARM INC.
XX Kastelic T, Cheneval D;
XX WPI; 2000-452406/39.
XX
PT Identifying compounds which affect mRNA stability for the treatment of
PT disease e.g. arthritis comprises a DNA expression system expressing a
PT protein having a detectable signal
XX
PS Disclosure; Fig 1; 31pp; English.
XX
CC This is the 3' UTR of interleukin 1-beta mRNA which contains AU-rich
CC element (ARE) motifs. These ARE motifs are found in genes subject to
CC mRNA instability. Identification of a compound which affects mRNA
CC stability comprises a DNA expression system which in the absence of the
CC test compound is capable of expressing a protein having a detectable
CC signal. The mRNA which codes for the protein, and which is transcribed
CC from the expression system, comprises at least one copy of a mRNA
CC instability sequence. The mRNA is contacted with a test compound and
CC the detectable signal is measured in the presence of the test compound
CC and compared with a control. Compounds identified by the new method can
CC be used for the treatment of a disease or medical condition which
CC involves inappropriate mRNA stabilization and/or accumulation and
CC undesirable protein expression (claimed) e.g. rheumatoid arthritis or
CC osteoarthritis.
XX
SQ Sequence 656 BP; 176 A; 151 C; 129 G; 200 T; 0 other;
Query Match 82.2%; Score 194; DB 21; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATGGTCTAATTTATTCAGAGGGGGCAAGTAGCAGTGTCTCTAAAGA 60
Db TTTTGATTCAATGGTCTAATTTATTCAGAGGGGGCAAGTAGCAGTGTCTCTAAAGA 488
QY 61 GCCTAGTTTAAATAGCTATGGAATCAATTTGAGTGGTGTCTCTCTTAAATC 120
Db GCCTAGTTTAAATAGCTATGGAATCAATTTGAGTGGTGTCTCTCTTAAATC 548
QY 121 AAGTCCTTTAATAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGATATTAT 180

|||||
Db 549 AAGTCCCTTTAATGAGACTGAAATATATATAAGCTCAGATATTAAATGGGAATATTAT 608
QY 181 AAATGAGCAAAATAT 194
Db 609 AAATGAGCAAAATAT 622
RESULT 3
AAF20946
ID AAF20946 standard; DNA; 1496 BP.
XX AAF20946;
AC AAF20946;
XX AAF20946;
DT 14-MAR-2001 (first entry)
XX Human interleukin-1 polynucleotide fragment #2513.
DE Human interleukin-1 polynucleotide fragment #2513.
XX Human interleukin-1 polynucleotide fragment #2513.
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosstatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX Homo sapiens.
OS Homo sapiens.
XX Homo sapiens.
PN WO200062736-A2.
XX WO200062736-A2.
PD 26-OCT-2000.
XX 26-OCT-2000.
PF 24-MAR-2000; 2000WO-US08020.
XX 24-MAR-2000; 2000WO-US08020.
PR 06-APR-1999; 99US-0127958.
XX 06-APR-1999; 99US-0127958.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX (NYCE/) NYCE J W.
PI Nyce JW;
XX Nyce JW;
DR WPI; 2000-679539/66.
XX WPI; 2000-679539/66.
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX cancers and respiratory obstructions -
PS Disclosure; Page 232-233; 1592pp; English.
XX Disclosure; Page 232-233; 1592pp; English.
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytosstatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX the present invention.
SQ Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;
Query Match 82.2%; Score 194; DB 21; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTTCATTGGTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60
Db 1269 TTTTGATTTCATTGGTCTAATTTATTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 1328
QY 61 GCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 120
Db 1329 GCTAGTTTTTAATAGCTATGGAATCAATTTCAATTTGGACTGGTGTCTCTTTAAATC 1388
QY 121 AAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 180
Db 1389 AAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 1448
QY 181 AAATGAGCAAAATAT 194
Db 1449 AAATGAGCAAAATAT 1462
RESULT 4
AAA34824
ID AAA34824 standard; DNA; 1496 BP.
XX AAA34824;
AC AAA34824;
XX AAA34824;
DT 28-JUL-2000 (first entry)
XX 28-JUL-2000 (first entry)
DE Human adenosine receptor related polynucleotide SEQ ID NO:2513.
XX Human adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS Homo sapiens.
XX Homo sapiens.
PN WO200009525-A2.
XX WO200009525-A2.
PD 24-FEB-2000.
XX 24-FEB-2000.
PF 03-AUG-1999; 99WO-US17712.
XX 03-AUG-1999; 99WO-US17712.
PR 03-AUG-1998; 98US-0095212.
XX 03-AUG-1998; 98US-0095212.
PA (UYEC-) UNIV EAST CAROLINA.
XX (UYEC-) UNIV EAST CAROLINA.
PI Nyce JW;
XX Nyce JW;
DR WPI; 2000-205971/18.
XX WPI; 2000-205971/18.
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX cancers -
PS Disclosure; Page 675; 1343pp; English.
XX Disclosure; Page 675; 1343pp; English.

XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing the
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX SQ Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;

Query Match 82.2%; Score 194; DB 21; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTTCATGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60
Db |||||
1269 TTTTGATTTCATGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 1328
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGAAGTGGTGTCTCTTTAAATC 120
Db |||||
1329 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGAAGTGGTGTCTCTTTAAATC 1388
QY 121 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
Db |||||
1389 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1448
QY 181 AAATGAGCAAAATAT 194
Db |||||
1449 AAATGAGCAAAATAT 1462

RESULT 5
AAN50060
ID AAN50060 standard; cDNA; 1507 BP.
XX
AC AAN50060;
XX
DT 09-SEP-1991 (first entry)
XX
DE Sequence encoding interleukin-1 (IL-1).
KW Immunological reagent; T cell stimulant; B cell; immunoglobulin; ss.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH 87..894
FT /*tag= a
FT

EP161901-A.
XX
XX 21-OCT-1985.
PD
XX 07-MAY-1985; 85EP-0303234.

XX 11-FEB-1985; 85US-0700374.
XX (NEW) NEW ENGLAND MED CEN.
XX
PI Auron PE, Webb AC, Gehrke L, Dinarello CA, Rosenwasser LJ, Rich A;
PI Wolff SM;
XX
DR WPI; 1985-291135/47.
DR P-PSDB; AAP50043.
XX
PT Recombinant cloning vehicle contg. human interleukin-7 gene-or its
PT fragments, producing new biologically active polypeptide(s)
XX
PS Claim 7; Page 34-35; 39pp; English.
XX
CC A pure cDNA of 1507 bp (AAN50060) (and its 1-606, 1-677, 1355-1507;
CC 482-1501; 482-677; and 1355-1507 fragments) are claimed. Also
CC claimed is a recombinant DNA cloning vehicle contg. the human IL-1
CC gene sequence. Specifically the vehicle contains the sequence coding
CC for the new 287 AA sequence (AAP50043) or the following new fragments
CC (1) 9-224; (2) 1-210-X; (3) 144-287; and (4) 144-210-(X); (X= Asn-
CC Ser-Ile-Trp-Thr-Gly-Val-Leu-Ser-Leu-Asn-Gln-Val-Leu).
XX
SQ Sequence 1507 BP; 427 A; 361 C; 328 G; 391 T; 0 other;

Query Match 82.2%; Score 194; DB 6; Length 1507;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTTCATGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60
Db |||||
1269 TTTTGATTTCATGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 1328
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGAAGTGGTGTCTCTTTAAATC 120
Db |||||
1329 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGAAGTGGTGTCTCTTTAAATC 1388
QY 121 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
Db |||||
1389 AAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 1448
QY 181 AAATGAGCAAAATAT 194
Db |||||
1449 AAATGAGCAAAATAT 1462

RESULT 6
AAQ50981
ID AAQ50981 standard; cDNA; 1507 BP.
XX
AC AAQ50981;
XX
DT 19-MAY-1994 (first entry)
XX
DE Human Interleukin-1 coding sequence.
KW hIL-1; interleukin; cytokine; truncated; N-terminal deletion;
KW C-terminal deletion; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 87..896
FT /*tag= a
FT /product= hIL-1
FT /note= "N- and C-terminally truncated forms of
FT this sequence which retain IL-1 activity
FT are covered by the invention"

EP569687-A.
XX
XX 18-NOV-1993.
PD

XX 07-MAY-1985; 85EP-0303234.
PF 18-MAY-1984; 84US-0611669.
PR 11-FEB-1985; 85US-0700374.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (NEWEN-) NEW ENGLAND MED. CENT HOSPITALS.
PA (TUFT) TUFTS COLLEGE.
PA (WELL-) WELLESLEY COLLEGE.
XX Auron PE, Dinarello CA, Gehrke L, Rich A, Rosenwasser LJ;
PI Webb AC, Wolff SM;
XX WPI; 1993-360975/46.
DR P-PSDB; AAR42213.
XX New DNA encoding protein with IL-1 activity - useful in
PT monitoring disease states e.g. cancer and studying inflammation
PT e.g. in arthritis etc.
XX Claim 1; Page 11-16; 24pp; English.
PS DNA comprising part of the nucleotide sequence AAQ50981 which encodes
CC a polypeptide having IL-1 activity and a mol.wt. of 20000 is claimed.
CC Specifically, the region between nucleotides 111-717 has been found
CC to retain hIL-1 activity (see AAQ45464).
XX Sequence 1507 BP; 427 A; 361 C; 328 G; 391 T; 0 other;
SQ Query Match 82.2%; Score 194; DB 14; Length 1507;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTGCTGCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGCTGTGTAAGA 60
Db 1269 TTTTGATTGCTGCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGCTGTGTAAGA 1328
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGCTCTCTTTAAATC 120
Db 1329 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGCTCTCTTTAAATC 1388
QY 121 AAGTCCTTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 180
Db 1389 AAGTCCTTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 1448
QY 181 AAATGAGCAAAATAT 194
Db 1449 AAATGAGCAAAATAT 1462
RESULT 7
AAX75924
ID AAX75924 standard; DNA; 9721 BP.
XX AAX75924;
AC AAX75924;
XX 29-JUL-1999 (first entry)
DT Human interleukin 1B gene.
XX Human; interleukin 1; IL-1B; IL-1A; IL-1RN; diagnosis; detection;
KW chronic obstructive airway disease; chronic bronchitis; emphysema;
KW asthma; chronic bronchiolitis; proinflammatory haplotype; ss.
XX Homo sapiens.
OS WO9924615-A2.
XX 20-MAY-1999.
PD 09-NOV-1998; 98WO-US23721.
XX

PR 12-JAN-1998; 98US-0005923.
PR 07-NOV-1997; 97GB-0023553.
XX (MEDI-) MEDICAL SCI SYSTEMS INC.
XX Barnes PJ, Duff GW, Giovine M, Lim S;
PI WPI; 1999-327420/27.
XX Genotyping nucleic acid samples for interleukin-1 (IL-1)
PT proinflammatory haplotype alleles, useful for predicting
PT susceptibility to developing chronic obstructive airway disease
XX Example 1; Fig 2; 37pp; English.
PS The present invention describes genotyping a nucleic acid sample from a
XX subject to determine at least one allele of an interleukin-1 (IL-1)
CC proinflammatory haplotype. A method has also been described for
CC determining a subject's susceptibility to developing chronic obstructive
CC airway disease (COAD) or for predicting the rapidity or ultimate
CC progression of a COAD in the subject by: (a) obtaining a nucleic acid
CC sample from the subject; and (b) detecting at least one allele of an
CC IL-1 proinflammatory haplotype in the sample, where detection of at
CC least one of these alleles indicates that the patient has an increased
CC susceptibility to developing COAD. The method is useful for determining
CC the susceptibility of subjects to developing chronic obstructive airway
CC disease or for predicting the rapidity or ultimate progression of
CC chronic obstructive airway disease (COAD). COAD can be asthma, emphysema,
CC chronic bronchitis or chronic bronchiolitis. The method provides for
CC early identification of chronic obstructive airway disease (COAD),
CC facilitating administration of appropriate treatment at the earliest
CC stage, thereby increasing the probability of a positive outcome. The
CC present sequence represents the human IL-1B gene.
XX
SQ Sequence 9721 BP; 2662 A; 2328 C; 2121 G; 2608 T; 2 other;
Query Match 82.2%; Score 194; DB 20; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTGCTGCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGCTGTGTAAGA 60
Db 8710 TTTTGATTGCTGCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGCTGTGTAAGA 8769
QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGCTCTCTTTAAATC 120
Db 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGCTCTCTTTAAATC 8829
QY 121 AAGTCCTTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 180
Db 8830 AAGTCCTTTTAATAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATTTAT 8889
QY 181 AAATGAGCAAAATAT 194
Db 8890 AAATGAGCAAAATAT 8903
RESULT 8
AAF20945
ID AAF20945 standard; DNA; 9721 BP.
XX AAF20945;
AC AAF20945;
XX 14-MAR-2001 (first entry)
DT Human interleukin-1 polynucleotide fragment #2512.
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

PF 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX Nyce JW;

PI WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -

XX Disclosure; Page 230-232; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

Query Match 82.2%; Score 194; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTTCATTGGTCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60

Db 8710 TTTTGATTTCATTGGTCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 8769

QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 120

Db 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 8829

QY 121 AAGTCCTTTAATAAGACTGAAATATATAAAGCTCAGATTATTTAAATGGGAATATTAT 180

Db 8830 AAGTCCTTTAATAAGACTGAAATATATAAAGCTCAGATTATTTAAATGGGAATATTAT 8889

QY 181 AAATGAGCAAAATAT 194

Db 8890 AAATGAGCAAAATAT 8903

RESULT 9

AAC63768

ID AAC63768 standard; DNA; 9721 BP.

XX AAC63768;

XX 08-FEB-2001 (first entry)

DE Human IL-1B gene.

XX Human; IL-1B; interleukin-1B; cytostatic; antiinflammatory;

KW immunosuppressive; dermatological; antimicrobial; antiarthritic;

KW IL-1 receptor antagonist; tumour necrosis factor alpha antagonist

KW interstitial lung disease; interstitial pneumonia; pulmonary fibrosis;

KW rheumatoid arthritis; systemic lupus erythematosis; Sjogren's syndrome;

KW systemic sclerosis; dermatomyocitis; chromosome 2; ds.

OS Homo sapiens.

XX WO200060117-A2.

PN 12-OCT-2000.

XX 31-MAR-2000; 2000WO-US08492.

XX 02-APR-1999; 99US-0286108.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Duff GW, Di Giovine FS, Whyte M;

XX WPI; 2000-656234/63.

XX Method for predicting the risk of interstitial lung disease, comprising
PT detecting an interleukin-1 receptor antagonist allele and tumor
PT necrosis alpha allele or an allele in linkage disequilibrium with
PT either of these alleles -

XX Claim 6; Fig 2; 102pp; English.

XX The present sequence is provided in a specification relating to a method
CC for determining whether a subject has or is predisposed to develop an
CC interstitial lung disease. The method involves detecting an interleukin-1
CC receptor antagonist (IL-1RN) (+2018) allele 2, a tumour necrosis alpha
CC (TNF-A)(-308) allele 2, or an allele in linkage disequilibrium with
CC either of these two alleles. The method may be used to determine whether
CC a subject has or is predisposed to develop an interstitial pneumonia or a
CC pulmonary fibrosis and other disorders such as rheumatoid arthritis,
CC systemic lupus erythematosis, Sjogren's syndrome, systemic sclerosis,
CC dermatomyocitis. The method is also used for identifying molecules
CC which can be used as therapeutics for treating interstitial lung disease.

XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

Query Match 82.2%; Score 194; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTTCATTGGTCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60

Db 8710 TTTTGATTTCATTGGTCTAATTTATTTCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 8769

QY 61 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 120

Db 8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 8829

QY 121 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
|||||
Db 8830 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 8889
QY 181 AAATGAGCAAAATAT 194
|||||
Db 8890 AAATGAGCAAAATAT 8903

RESULT 10
AAA50174
ID AAA50174 standard; DNA; 9721 BP.
XX
AC AAA50174;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human interleukin-1 beta allele 1 (+6912).
XX
KW Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;
KW coronary artery disease; osteoporosis; nephropathy;
KW alopecia areata; Graves disease; systemic lupus erythematosus;
KW lichen sclerosis; ulcerative colitis; diabetic retinopathy;
KW periodontal disease; juvenile chronic arthritis; psoriasis;
KW insulin dependent diabetes; asthma; lung fibrosis;
KW chronic inflammatory liver disease; rheumatoid arthritis;
KW chronic inflammatory lung disease; antiinflammatory; osteopathic;
KW dermatological; immunosuppressive; antidiabetic; antithyroid;
KW antiarthritic; antirheumatic; antiasthmatic; antipsoriatic;
KW hepatotropic; antiulcer; diagnosis; therapy; ds.

XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT variation replace(8904,G)
FT /*tag= a
FT /note= "IL-1B allele 1 (+6912)"

XX WO200047619-A1.
XX
XX 17-AUG-2000.
XX
XX 10-FEB-2000; 2000WO-US03443.
XX
XX 10-FEB-1999; 99US-0247874.
XX (INTE-) INTERLEUKIN GENETICS INC.
XX
XX Duff GW, Di Giovine FS;
XX
XX WPI; 2000-558192/51.
XX
XX Novel methods and nucleic acids for diagnosing and treating disorders
XX associated with high levels of interleukin 1beta, especially
XX inflammatory diseases -
XX
XX Disclosure; Fig 1; 74pp; English.

XX The present sequence is that of human interleukin-1 beta (IL-1B)
XX allele 1 (+6912), which is a form of the IL-1B gene that contains
XX cytosine at position +6912; IL-1B allele 2 (+6912) has guanine at
XX this position (see AAA50175). The invention is based on the
XX identification of this novel allele at marker +6912 of the IL-1B
XX gene. The C to G transition occurs within the 3' untranslated
XX region of the IL-1B gene and results in an increased level of IL-1B
XX protein. Individuals homozygous for the IL-1B allele 2 (+6912)
XX accumulate approximately 4 times more immunoreactive IL-1B protein
XX than homozygotes for IL-1B allele 1 (+6912). Methods and kits are
XX provided for detecting IL-1B allele 2 (+6912), or an allele in
XX linkage disequilibrium with an IL-1B allele 2 (+6912), and
XX thereby determining a patient's susceptibility to developing
XX inflammatory disorders, especially coronary artery disease,

CC osteoporosis, nephropathy in diabetes mellitus, alopecia areata,
CC Graves disease, systemic lupus erythematosus, lichen sclerosis,
CC ulcerative colitis, diabetic retinopathy, periodontal disease,
CC juvenile chronic arthritis, psoriasis, insulin dependent diabetes,
CC asthma, chronic inflammatory liver disease, chronic inflammatory
CC lung disease, lung fibrosis, and rheumatoid arthritis (claimed).
CC Identification of the IL-1B allele 2 (+6912) and its involvement in
CC IL-1B overproduction also enables screening assays for identifying
CC IL-1B antagonists that can be used to treat conditions associated
CC with IL-1B allele 2 (+6912). Transgenic animals are also claimed,
CC and can be used to identify IL-1B agonists and antagonists, or
CC to confirm the safety and efficacy of candidate therapeutics.

XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
Query Match 82.2%; Score 194; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGATTCAATTGGTCTAATTTATTCAAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 60
|||||
Db 8710 TTTTGATTCAATTGGTCTAATTTATTCAAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 8769
QY 61 GCCTAGTTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATC 120
|||||
Db 8770 GCCTAGTTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATC 8829
QY 121 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 180
|||||
Db 8830 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTAT 8889
QY 181 AAATGAGCAAAATAT 194
|||||
Db 8890 AAATGAGCAAAATAT 8903

RESULT 11
AAA34823
ID AAA34823 standard; DNA; 9721 BP.

XX
XX AAA34823;
XX
XX 28-JUL-2000 (first entry)
XX
XX Human adenosine receptor related polynucleotide SEQ ID NO:2512.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17712.
XX
XX 03-AUG-1998; 98US-0095212.
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers
XX
PS Disclosure; Page 673-675; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX

Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

Query Match 82.2%; Score 194; DB 21; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTGATTCAATGGTCTAATTATTCAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 60
Db 8710 TTTTGATTCAATGGTCTAATTATTCAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 8769
OY 61 GCCTAGTTTAAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 120
Db 8770 GCCTAGTTTAAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 8829
OY 121 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTAT 180
Db 8830 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTAT 8889
OY 181 AAATGAGCAAAATAT 194
Db 8890 AAATGAGCAAAATAT 8903

RESULT 12
AAF27666
ID AAF27666 standard; DNA; 9721 BP.
XX
AC AAF27666;
XX
DT 02-APR-2001 (first entry)
XX
DE IL-1B DNA.
XX
KW IL-1; interleukin; inflammation; infection; ds.
XX
OS Unidentified.
XX
PN WO200100880-A2.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18318.

XX 30-JUN-1999; 99US-0345217.
XX (INTE-) INTERLEUKIN GENETICS INC.
PA Duff GW, Cox A, Camp NJ, Di Giovine FS;
XX WPI; 2001-102903/11.
PT Determining whether a subject has or is predisposed to disease
PT associated with IL-1 polymorphism involves determining presence of
PT marker or allele comprising IL-1 inflammatory haplotype -
XX Disclosure; Fig 4; 84pp; English.
XX
CC The present invention relates to a new method for determining whether
CC a subject has or is predisposed to developing a disease or condition
CC that is associated with an IL (interleukin)-1 inflammatory haplotype,
CC comprises detecting at least one allele of the haplotype, where the
CC presence of the allele indicates that the subject is predisposed to
CC the development or has the disease or condition.
CC The method is useful for determining whether a subject has or is
CC predisposed to inflammatory disease, a degenerative disease, an
CC immunological disorder, an infectious disease, trauma induced disease,
CC or cancer. The above conditions associated with an IL-1 inflammatory
CC haplotype can be treated or prevented by administering a therapeutic
CC that compensates for a causative mutation that is in linkage
CC disequilibrium with at least one IL-1 polymorphism.
XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2607 T; 3 other;

Query Match 82.2%; Score 194; DB 22; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTGATTCAATGGTCTAATTATTCAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 60
Db 8710 TTTTGATTCAATGGTCTAATTATTCAAGGGGGCAAGTAGCAGTGTCTGTAAAGA 8769
OY 61 GCCTAGTTTAAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 120
Db 8770 GCCTAGTTTAAATAGCTATGGAATCAATTCAATTTGGACTGGTGTCTCTTTAAATC 8829
OY 121 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTAT 180
Db 8830 AAGTCCTTTAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTAT 8889
OY 181 AAATGAGCAAAATAT 194
Db 8890 AAATGAGCAAAATAT 8903

RESULT 13
AAC91434
ID AAC91434 standard; DNA; 9721 BP.
XX
AC AAC91434;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human IL-1B nucleotide sequence.
XX
KW Human; IL-1A; interleukin-1alpha; IL-1B; interleukin-1beta; IL-1RN;
KW interleukin-1 receptor antagonist; vasotropic; antiinflammatory;
KW hypotensive; anticoagulant; antilipemic; arterial restenosis;
KW restenosis associated allele; RAA; occlusive cardiovascular disorder;
KW restenosis detection; ds.
XX
OS Homo sapiens.
XX
PN WO200071753-A2.
XX
PD 30-NOV-2000.

XX	24-MAY-2000; 2000WO-US14299.
PF	
XX	
PR	24-MAY-1999; 99US-0317674.
PR	01-NOV-1999; 99US-0431352.
XX	
PA	(INTE-) INTERLEUKIN GENETICS INC.
XX	
PI	Kornman KS, Duff GW, Crossman D
XX	
DR	WPI; 2001-025173/03.

The present sequence is given in a specification relating to a method for determining whether a subject has or is predisposed to developing an arterial restenosis. The method comprises detecting a restenosis associated allele (RAA) in a nucleic acid sample from the subject, where detection of the RAA indicates that the subject has or is predisposed to the development of a restenosis. The restenosis associated allelic pattern permits the diagnosis of occlusive cardiovascular disorder. The diagnosis allows the most suitable treatment methods for restenosis to be used e.g. selecting therapies for initial vascular stenosis most likely to avoid subsequent stenoses. The detection methods identify restenosis therapeutics, agonists and antagonists, (proteins, peptides, peptidomimetics, small molecules or nucleic acids, e.g. anti-sense, ribozyme and triplex nucleic acids) which are used to treat restenosis.

12-SEP-2001; 2001WO-US28465.
12-SEP-2000; 2000US-231785P.
(BGHM) BRIGHAM & WOMENS HOSPITAL INC.
(DAND) DANA FARBER CANCER INST INC.
Hill JA, Wang ZC, Anderson DJ, Yunis EJ;
WPI; 2002-362362/39.
Evaluating risk of unexplained recurrent pregnancy loss in a subject,
by testing presence of a variant in interleukin-1 beta promoter region
and/or in CD46 gene intron 1 region in a sample obtained from the
subject -
Example 2 and 3; Page 51-54; 57pp; English.
The invention relates to a method for evaluating and treating risk of
unexplained recurrent pregnancy loss (URPL) in a subject suspected of
having immunologic reproductive failure. The method involves testing a
sample obtained from the subject for the presence of a variant in the
human interleukin-1beta (IL-1beta) promoter region, and/or a variant
in the CD46 gene intron 1 region, where the presence of the variant,
indicates an elevated risk of developing recurrent pregnancy loss.
The present sequence is human prointerleukin-1 beta (IL-1 beta) gene.
Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

```

Query Match      82.2%; Score 194; DB 24; Length 9721;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY	1	TTTTGATTCAATGGTCTCAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAGA	60
Db	8710	TTTTGATTCAATGGTCTCAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAGA	8769
QY	61	GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTGCTCTCTTTAAATC	120
Db	8770	GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTGGACTGGTGTGCTCTCTTTAAATC	8829
QY	121	AAGTCCTTTAATTAAGACTGAAATATATAAGCTCACATTATTTAAATGGGAATATTTAT	180
Db	8830	AAGTCCTTTAATTAAGACTGAAATATATAAGCTCACATTATTTAAATGGGAATATTTAT	8889
QY	181	AAATGAGCAAAATAT	194
Db	8890	AAATGAGCAAAATAT	8903

RESULT 15
AAF20950
ID AAF20950 standard; DNA; 29433 BP.
XX AC AAF20950;
XX AC
XX DT 14-MAR-2001 (first entry)
XX DE Human interleukin-1 polynucleotide fragment #2517.
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX KW
OS Homo sapiens.

Search completed: March 17, 2003, 20:46:15
Job time : 257 secs

XX WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 221-227; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 2 other;

Query Match 82.2%; Score 194; DB 21; Length 29433;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTTCATTGGTCTAATTTATCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 60
Db 22177 TTTTGATTTCATTGGTCTAATTTATCAAGGGGGCAAGAGTAGCAGTGTCTGTAAAGA 22236

QY 61 GCCTAGTTTTTAATAGCTATGGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATC 120
Db 22237 GCCTAGTTTTTAATAGCTATGGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATC 22296

QY 121 AAGTCCTTTAATTAAGACTGAAATATATATAGCTCAGATTATTTAAATGGGAATTTAT 180
Db 22297 AAGTCCTTTAATTAAGACTGAAATATATATAGCTCAGATTATTTAAATGGGAATTTAT 22356

QY 181 AAATGAGCAAAATAT 194
Db 22357 AAATGAGCAAAATAT 22370

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 20:34:55 ; Search time 1462 Seconds
(without alignments)
2614.319 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
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9: gb_est1:*
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11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
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22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	189	80.1	324	9 AA923615	AA923615 nq98b03.s
C 2	189	80.1	413	14 W38319	W38319 zc77b02.s1
C 3	189	80.1	514	9 AA131744	AA131744 z135f02.s
C 4	189	80.1	521	9 AI022364	AI022364 ow64g05.x
C 5	189	80.1	528	9 AI678441	AI678441 tu82d01.x
C 6	189	80.1	548	14 BM997237	BM997237 UI-H-DH0-

C 7	189	80.1	554	9 AA577318	AA577318 nm89a08.s
C 8	189	80.1	618	10 AW273081	AW273081 xu27h01.x
C 9	189	80.1	703	14 BQ001221	BQ001221 UI-H-DH1-
C 10	189	80.1	770	14 BQ000281	BQ000281 UI-H-DP0-
C 11	189	80.1	817	9 AI609005	AI609005 tw85g07.x
C 12	189	80.1	911	12 BG194765	BG194765 RST14064
C 13	147	62.3	549	9 AI566931	AI566931 tq67h02.x
C 14	147	62.3	746	13 BI519707	BI519707 603061928
C 15	143	60.6	793	14 BM999417	BM999417 UI-H-DP0-
C 16	138	58.5	314	9 AA382165	AA382165 EST95328
C 17	138	58.5	375	12 BG119263	BG119263 602349136
C 18	138	58.5	698	9 AI471571	AI471571 t198h09.x
C 19	136	57.6	429	14 T29172	T29172 EST71708.Hu
C 20	130	55.1	415	9 AA362146	AA362146 EST71810
C 21	130	55.1	749	12 BG117168	BG117168 602346446
C 22	125	53.0	454	14 D20737	D20737 HUMGS01714
C 23	124	52.5	223	9 AA362379	AA362379 EST71836
C 24	113	47.9	619	10 AW953756	AW953756 EST365826
C 25	108	45.8	430	14 W47101	W47101 zc39b04.s1
C 26	107	45.3	196	9 AA362067	AA362067 EST71531
C 27	97	41.1	241	14 C06317	C06317 C06317 Huma
C 28	93	39.4	286	10 BE183186	BE183186 RC4-HT066
C 29	61	25.8	925	10 BE619601	BE619601 601472701
C 30	51	21.6	252	10 AW779422	AW779422 hn94a09.x
C 31	31	13.1	259	12 BG058513	BG058513 naf15e02.
C 32	28	11.9	265	10 BE183137	BE183137 RC4-HT066
C 33	24	10.2	703	10 AV715551	AV715551 AV715551
C 34	23	9.7	360	9 AA916006	AA916006 oh86h07.s
C 35	22	9.3	559	17 BH598295	BH598295 BOHCP37TR
C 36	20	8.5	685	17 AG163910	AG163910 Pan trogl
C 37	20	8.5	993	17 CNS060CR	AL407905 T7 end of
C 38	19	8.1	300	14 C53301	C53301 C53301 Yuji
C 39	19	8.1	381	17 AZ236878	AZ236878 RPCI-23-9
C 40	19	8.1	463	13 BJ148984	BJ148984 BJ148984
C 41	19	8.1	476	14 BM864065	BM864065 mgcm008xB
C 42	19	8.1	583	17 BH674814	BH674814 BOMEG17TR
C 43	19	8.1	616	17 AQ436473	AQ436473 HS_5052_B
C 44	19	8.1	646	12 BG809864	BG809864 mgct001xm
C 45	19	8.1	661	10 AV702246	AV702246 AV702246

ALIGNMENTS

RESULT 1
AA923615/c 324 bp mRNA linear EST 29-APR-1998
LOCUS nq98b03.s1 NCI CGAP Col0 Homo sapiens cDNA clone IMAGE:1160333 3'
DEFINITION similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AA923615
VERSION AA923615.1 GI:3070924
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1123 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 214.

FEATURES
source

Location/Qualifiers
1. .324
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1160333"
/clone_lib="NCI CGAP Col0"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."

BASE COUNT 117 a 55 c 57 g 95 t
ORIGIN

Query Match 80.1%; Score 189; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 7e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
Db 227 ATTCATTGGTCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 168
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 125
Db 167 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 108
QY 126 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
Db 107 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 48
QY 186 AGCAAATAT 194
Db 47 AGCAAATAT 39

RESULT 2
W38319/c
LOCUS
DEFINITION
W38319 413 bp mRNA linear EST 15-MAY-1996
zc77b02.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328299 3', similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION W38319
VERSION W38319.1 GI:1319934
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

TITLE
JOURNAL
MEDLINE
COMMENT

Seq primer: mob.REGA+ET
High quality sequence stop: 368.

FEATURES
source

Location/Qualifiers
1. .413
/organism="Homo sapiens"
/db_xref="GDB:1262503"
/db_xref="taxon:9606"
/clone="IMAGE:328299"
/clone_lib="Pancreatic Islet"
/tissue_type="pancreatic islet"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993) Takeda et al. Cloned unidirectionally. Primer: Oligo dT. ~5' adaptor sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3' "

BASE COUNT 135 a 65 c 86 g 127 t
ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 413;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
Db 239 ATTCATTGGTCTAAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 180
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 125
Db 179 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 120
QY 126 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
Db 119 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 60
QY 186 AGCAAATAT 194
Db 59 AGCAAATAT 51

RESULT 3
AA131744/c
LOCUS

DEFINITION
AA131744 514 bp mRNA linear EST 27-NOV-1996
2135f02.s1 Soares_pregnant_uterus NBHPU Homo sapiens cDNA clone IMAGE:503931 3', similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA131744
VERSION AA131744.1 GI:1693270
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 514)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 277.

FEATURES
source

Location/Qualifiers
1. .514
/organism="Homo sapiens"

/db_xref="GDB:3808919"
/db_xref="taxon:9606"
/clone="IMAGE:503931"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5,
AACTGGAAGAAATCGCGGCCGCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

BASE COUNT 156 a 85 c 114 g 149 t 10 others
ORIGIN
Query Match 80.1%; Score 189; DB 9; Length 514;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAATTATTCAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 244 ATTCATTGGTCTAATTATTCAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 185
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
|||||
Db 184 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
QY 126 CTTTAAATTAAGCTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
|||||
Db 124 CTTTAAATTAAGCTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 65
QY 186 AGCAAATAT 194
|||||
Db 64 AGCAAATAT 56

RESULT 4
AI022364/c
LOCUS
DEFINITION
ow64g05.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
clone IMAGE:1651640 3', similar to gb:M15330 INTERLEUKIN-1 BETA
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
AI022364
VERSION
AI022364.1 GI:3237605
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 521)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1077 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 403.
Location/Qualifiers
1. .521
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1651640"
/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"

FEATURES
source
1. .521
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1651640"
/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"

/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V type: phagemid; Site 1: Not I; Site 2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5,
TGTACCAATCTGAAGTGGAGCGCGCATTTT 3'];
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 165 a 92 c 123 g 141 t
ORIGIN

Query Match 80.1%; Score 189; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAATTATTCAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 232 ATTCATTGGTCTAATTATTCAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 173
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
|||||
Db 172 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 113
QY 126 CTTTAAATTAAGCTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 185
|||||
Db 112 CTTTAAATTAAGCTGAAATATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG 53
QY 186 AGCAAATAT 194
|||||
Db 52 AGCAAATAT 44

RESULT 5
AI678441/c
LOCUS
DEFINITION
tu82d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2257537 3',
similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION
AI678441
VERSION
AI678441.1 GI:4888623
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1763 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 404.
Location/Qualifiers
1. .528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2257537"
/clone_lib="NCI CGAP Gas4"
/tissue_type="poorly differentiated adenocarcinoma with

FEATURES
source
1. .528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2257537"
/clone_lib="NCI CGAP Gas4"
/tissue_type="poorly differentiated adenocarcinoma with

signet ring cell features"

/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

BASE COUNT 172 a 98 c 117 g 140 t 1 others
ORIGIN

Query Match 80.1%; Score 189; DB 9; Length 528;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 227 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 168
|||||
QY 66 GTTTTAAATAGCTATGGAATCAATTCGAATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 125
|||||
Db 167 GTTTTAAATAGCTATGGAATCAATTCGAATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 108
|||||
QY 126 CTTTAAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTATATAAATG 185
|||||
Db 107 CTTTAAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTATATAAATG 48
|||||
QY 186 AGCAAATAT 194
|||||
Db 47 AGCAAATAT 39
|||||

RESULT 6

BM997237/c
LOCUS BM997237 548 bp mRNA linear EST 17-JUN-2002
DEFINITION UI-H-DHO-auc-f-03-0-UI.s1 NCI_CGAP_DHO Homo sapiens cDNA clone
IMAGE:5872130 3', mRNA sequence.

ACCESSION BM997237
VERSION BM997237.1 GI:19722138
KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 548)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

The following repetitive elements were found in this cDNA

sequence: 221-272, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

FEATURES

source

Location/Qualifiers

1..548
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5872130"
/clone_lib="NCI_CGAP_DHO"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_DHO is a cDNA library containing the following
tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma
in Lung. The library was constructed according to Bonaldo,

Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGATCATTCG.

TAG LIB=UI-H-DHO

TAG_TISSUE=lung

TAG_SEQ=AGATCATTCG"

BASE COUNT 172 a 95 c 123 g 158 t
ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 548;
Best Local Similarity 100.0%; Pred. No. 7.5e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 242 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAGAGCCTA 183
|||||
QY 66 GTTTTAAATAGCTATGGAATCAATTCGAATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 125
|||||
Db 182 GTTTTAAATAGCTATGGAATCAATTCGAATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 123
|||||
QY 126 CTTTAAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTATATAAATG 185
|||||
Db 122 CTTTAAATTAAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTATATAAATG 63
|||||

QY 186 AGCAAATAT 194
|||||

Db 62 AGCAAATAT 54
|||||

RESULT 7

AA577318/c

LOCUS

DEFINITION

AA577318 554 bp mRNA linear EST 12-SEP-1997
nm89a08.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1075382 3'
similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.

ACCESSION AA577318

VERSION AA577318.1 GI:2354792

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 554)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.

, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert length: 1351 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 414.

Location/Qualifiers

source

1..554

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1075382"

/clone_lib="NCI_CGAP_Co9"

/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Ronaldo (Soares4).

BASE COUNT 176 a 97 c 126 g 154 t 1 others
ORIGIN
Query Match 80.1%; Score 189; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 7.5e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAATTATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
Db 231 ATTCATTGGTCTAATTATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 172
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 125
Db 171 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 112
QY 126 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTATATAATG 185
Db 111 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTATATAATG 52
QY 186 AGCAAATAT 194
Db 51 AGCAAATAT 43

RESULT 8
AW273081/c
LOCUS
DEFINITION xu27h01.x1 NCI CGAP_Col4 Homo sapiens cDNA clone IMAGE:2801425 3' similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AW273081.1 GI:6660111
VERSION EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 618)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.; Ph.D., Michael R. Emmert-Buck, M.D.; Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 399.
Location/Qualifiers
1. .618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2801425"
/clone_lib="NCI_CGAP_Col4"

FEATURES
source

/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Life Technologies catalog #:

BASE COUNT 193 a 121 c 137 g 167 t
ORIGIN
Query Match 80.1%; Score 189; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 7.6e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
Db 227 ATTCATTGGTCTAATTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 168
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
Db 167 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 108
QY 126 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTATATAATG 185
Db 107 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTATATAATG 48
QY 186 AGCAAATAT 194
Db 47 AGCAAATAT 39

RESULT 9
BQ001221/c
LOCUS
DEFINITION UI-H-DH1-awp-g-21-0-UI.s1 NCI_CGAP_DH1 Homo sapiens cDNA clone IMAGE:5892524 3', mRNA sequence.
ACCESSION BQ001221
VERSION BQ001221.1 GI:19726121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 703)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA sequence: 221-272, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1. .703
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5892524"
/clone_lib="NCI_CGAP_DH1"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTCG.

TAG_LIB=UI-H-DH1
TAG_TISSUE=lung
TAG_SEQ=AGATCATTCG

BASE COUNT 203 a 139 c 158 g 202 t 1 others
ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 703;
Best Local Similarity 100.0%; Pred. No. 7.7e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 242 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 183
|||||
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 125
|||||
Db 182 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 123
|||||
QY 126 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
|||||
Db 122 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 63
|||||
QY 186 AGCAAATAT 194
|||||
Db 62 AGCAAATAT 54

RESULT 10
BQ000281/c
LOCUS
DEFINITION UI-H-DPO-avt-c-13-0-UI.s1 NCI CGAP_Fs1 Homo sapiens cDNA clone
IMAGE:5883972 3', mRNA sequence.

ACCESSION BQ000281 GI:19725181
VERSION BQ000281
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 770)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 221-272. >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1..770
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5883972"
/clone_lib="NCI CGAP_Fs1"
/tissue_type="Fibrosarcoma"
/lab_host="DH10B (Life Technologies)"

/note="Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_Fs1 is a cDNA library containing the following tissue(s): Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTCTACGAG.

TAG_LIB=UI-H-DPO
TAG_TISSUE=fibrosarcoma
TAG_SEQ=GTTCTACGAG

BASE COUNT 218 a 148 c 177 g 224 t 3 others
ORIGIN

Query Match 80.1%; Score 189; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 7.8e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
|||||
Db 242 ATTCATTGGTCTAATTTATTCAAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCTA 183
|||||
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 125
|||||
Db 182 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTCTTTAAATCAAGTC 123
|||||
QY 126 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
|||||
Db 122 CTTTAAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 63
|||||
QY 186 AGCAAATAT 194
|||||
Db 62 AGCAAATAT 54

RESULT 11
AI609005/c
LOCUS
DEFINITION AI609005 817 bp mRNA linear EST 15-DEC-1999
tw85g07.x1 NCI CGAP HN5 Homo sapiens cDNA clone IMAGE:2266524 3',
similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.

ACCESSION AI609005
VERSION AI609005.1 GI:4618172
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NCI/NIH-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chong Heon Lee, D.D.S., Mary May, J. Silvio
Gutkind, Ph.D., Myung Hee Park, PhD.
cDNA Library Preparation: Stratagene, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1651 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 441
POLYA=No.

FEATURES
source

Location/Qualifiers
1. .817
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2266524"
/clone_lib="NCI_CGAP_HN5"
/tissue_type="normal gingiva (cell line from primary keratinocytes)"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI
; Cloned unidirectionally. Primer: Oligo dT. Average
insert size 1.3 kb. 5' adaptor sequence: 5' AATTCGGCAGG
3' GCCGTGCTC 5' 3' adaptor
sequence: 5' (GA)10ACTAGTCTCGAGTTTTTTTTTTTTTTT 3' EcoRI
site appears to have been lost in a fraction of the
clones. Library constructed by Stratagene; available
through Mary May, PhD (Oral and Pharyngeal Cancer Branch,
National Institute of Dental and Craniofacial Research,
NIH; mmay@yoda.nidr.nih.gov)."

BASE COUNT 230 a 163 c 187 g 231 t 6 others
ORIGIN

Query Match 80.1%; Score 189; DB 9; Length 817;
Best Local Similarity 100.0%; Pred. No. 7.9e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAAGAGCCTA 65
|||||

Db 229 ATTCATTGGTCTAATTATTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAAGAGCCTA 170
|||||

QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
|||||

Db 169 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 110
|||||

QY 126 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
|||||

Db 109 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 50
|||||

QY 186 AGCAAAATAT 194
|||||

Db 49 AGCAAAATAT 41
|||||

RESULT 12
BG194765/c
LOCUS RST14064 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence. EST 21-APR-2001
DEFINITION BG194765
ACCESSION BG194765
VERSION BG194765.1 GI:13716580
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 911)

REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
, E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
, J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 434.

FEATURES
source
Location/Qualifiers
1. .911

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 254 a 184 c 219 g 254 t
ORIGIN

Query Match 80.1%; Score 189; DB 12; Length 911;
Best Local Similarity 100.0%; Pred. No. 8e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTATTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAAGAGCCTA 65
|||||

Db 229 ATTCATTGGTCTAATTATTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAAGAGCCTA 170
|||||

QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
|||||

Db 169 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 110
|||||

QY 126 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 185
|||||

Db 109 CTTTAAATTAAGACTGAAATATATATAAGCTCAGATTATTAAATGGGAATATTATAAATG 50
|||||

QY 186 AGCAAAATAT 194
|||||

Db 49 AGCAAAATAT 41
|||||

RESULT 13
AI566931/c
LOCUS tq67h02.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone linear EST 13-MAY-1999
DEFINITION similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AI566931
VERSION AI566931.1 GI:4525383
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 549)

REFERENCE
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1104 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 409
POLYA=No.

FEATURES
source
Location/Qualifiers
1. .549
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2213907"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly

differentiated (4 pooled tumors, including primary and metastatic)"
/dev stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 173 a 107 c 119 g 149 t 1 others
ORIGIN

Query Match 62.3%; Score 147; DB 9; Length 549;
Best Local Similarity 100.0%; Pred. No. 9.1e-70;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TGTCTGTAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTG 107
|||||
Db 186 TGTCTGTAAGAGCCCTAGTTTTTAATAGCTATGGAATCAATTCATTTGGACTGGTGTG 127
|||||

QY 108 CTCTCTTTAAATCAAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTATTTAAA 167
|||||
Db 126 CTCTCTTTAAATCAAGTCCTTTTAATAGACTGAAATATATATAAGCTCAGATTATTTAAA 67
|||||

QY 168 TGGGAATATTATATAAATGAGCAATAT 194
|||||
Db 66 TGGGAATATTATATAAATGAGCAATAT 40
|||||

RESULT 14
BI519707/c
LOCUS BI519707 746 bp mRNA linear EST 29-AUG-2001
DEFINITION 603061928T1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211294 3', mRNA sequence.

ACCESSION BI519707
VERSION BI519707.1 GI:15344499
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 746)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11530 Row: g column: 07
High quality sequence start: 3
High quality sequence stop: 740.

FEATURES
source
1..746
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5211294"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 206 a 158 c 177 g 205 t
ORIGIN

Query Match 62.3%; Score 147; DB 13; Length 746;
Best Local Similarity 100.0%; Pred. No. 9.5e-70;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTTATTCAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCCTA 65
|||||
Db 148 ATTCATTGGTCTAATTTATTCAAGGGGCAAGAGTAGCAGTGTCTGTAAAGAGCCCTA 89
|||||

QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 125
|||||
Db 88 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTCTCTTTAAATCAAGTC 29
|||||

QY 126 CTTTAATTAAGACTGAAATATATAAG 152
|||||
Db 28 CTTTAATTAAGACTGAAATATATAAG 2
|||||

RESULT 15
BM999417/c
LOCUS BM999417 793 bp mRNA linear EST 17-JUN-2002
DEFINITION UI-H-DPO-avf-1-11-0-UI.s1 NCI_CGAP_Fs1 Homo sapiens cDNA clone IMAGE:5878810 3', mRNA sequence.

ACCESSION BM999417
VERSION BM999417.1 GI:19724318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 793)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA sequence: 219-270. >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..793
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5878810"
/clone_lib="NCI_CGAP_Fs1"
/tissue_type="Fibrosarcoma"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_Fs1 is a cDNA library containing the following tissue(s): Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains

a library tag sequence that is located between the Not I site and the (dt)18 tail. The sequence tag for this library is GTTCTACGAG.

TAG_LIB=UI-H-DP0
TAG_TISSUE=fibrosarcoma
TAG_SEQ=GTTCTACGAG"

BASE COUNT 224 a 154 c 181 g 231 t 3 others
ORIGIN

Query Match 60.6%; Score 143; DB 14; Length 793;
Best Local Similarity 100.0%; Pred.No. 1.5e-67;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAAGAGCCTA 65
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAGTAGCAGTGTCTGTAAAAGAGCCTA 181
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 66 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTTAAATCAAGTC 125
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180 GTTTTAAATAGCTATGGAATCAATTCATTTGGACTGGTGTGCTCTCTTTAAATCAAGTC 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 126 CTTTAATTAAGACTGAAAATATA 148
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 120 CTTTAATTAAGACTGAAAATATA 98
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: March 17, 2003, 21:29:38
Job time : 1464 secs

